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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:13:34 ; Search time 9586 Seconds
(without alignments)
17560.049 Million cell updates/sec

Title: US-09-919-770-3

Perfect score: 5784

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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- 3: gb_in.*
- 4: gb_cm.*
- 5: gb_ov.*
- 6: gb_pat.*
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- 8: gb_pl.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
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| 2 | 5784 | 100.0 | 5784 | 6 | AX375587 | AX375587 Sequence |
| 3 | 5784 | 100.0 | 5784 | 6 | AX409513 | AX409513 Sequence |
| 4 | 5784 | 100.0 | 5784 | 6 | AX480837 | AX480837 Sequence |
| 5 | 5784 | 100.0 | 5784 | 9 | HUMTHRSPO | L12350 Human thrm |
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| 12 | 1604.2 | 27.7 | 5269 | 4 | AB005287 | AB005287 Bos tauru |
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| 14 | 1550.4 | 26.8 | 5722 | 6 | AX411057 | AX411057 Sequence |
| 15 | 1550.4 | 26.8 | 5722 | 9 | HSTS | X14787 Human mRNA |
| 16 | 1550.4 | 26.8 | 5724 | 6 | AX480835 | AX480835 Sequence |
| 17 | 1548.8 | 26.8 | 4434 | 9 | HSTHROMR | X04665 Human mRNA |
| 18 | 1548.8 | 26.8 | 7232 | 6 | AX281758 | AX281758 Sequence |
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| 20 | 1522.2 | 26.3 | 4339 | 10 | MUSTSP1A | M87276 Mouse thrm |
| 21 | 1335.4 | 23.1 | 3522 | 5 | XELSTAGE | L04278 Xenopus lae |
| 22 | 1139.4 | 19.7 | 1559 | 4 | BTRNAT3 | X87620 B.taurus mr |
| 23 | 904 | 15.6 | 2162 | 4 | BTRNAT1 | X87618 B.taurus mr |
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| 25 | 617.6 | 10.7 | 2302 | 4 | AF325902 | AF325902 Equus cab |
| 26 | 605.4 | 10.5 | 2438 | 10 | AF033530 | AF033530 Mus muscu |
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| 37 | 566.6 | 9.8 | 2061 | 9 | BC018786 | BC018786 Homo sapi |
| 38 | 566.6 | 9.8 | 3145 | 10 | MUSTSP3 | L04302 Mouse thrm |
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ALIGNMENTS

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LOCUS AX330488 5784 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 997 from Patent WO0194629.
ACCESSION AX330488
VERSION AX330488.1 GI:18103466
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrikan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature

QY 1981 TCTTGGCAATGACACCACTGTGAGGACCTGGACGAGTGTGCCCTGGTCCCGGACATCT 2040
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ACCESSION AX375587
VERSION    AX375587.1
KEYWORDS   GI:19170155
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MARTINSON,L.D. and SCATENA,M.
Methods and devices to modulate the wound response
Patent: WO 0209735-A 3 07-FEB-2002;
The University of Washington (US)
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ORIGIN

Query Match 100.0%; Score 5784; DB 6; Length 5784;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 721 | ACAGCTTGCAGTGGGCTGCACTCATAGGACAGTTCGCTGAGGAGGCGCTTCTACG | 780 |
| Db | 721 | ACAGCTTGCAGTGGGCTGCACTCATAGGACAGTTCGCTGAGGAGGCGCTTCTACG | 780 |
| QY | 781 | AGCACCTGCAGGCGGAAAGACCGGATGTACGTGGCCAAAGCTCTGCCAGAGAGATC | 840 |
| Db | 781 | AGCACCTGCAGGCGGAAAGACCGGATGTACGTGGCCAAAGCTCTGCCAGAGAGATC | 840 |

| | | | |
|----|------|---|------|
| Db | 781 | AGCACCTGCAGGCGGAAAGACCGGATGTACGTGGCCAAAGCTCTGCCAGAGAGATC | 840 |
| QY | 841 | ACTTACAGGGTGTGCTTTCAGAAAGCTCCACCTAGTGTGTTGAAAACCTCTGTGGAAGATATC | 900 |
| Db | 841 | ACTTACAGGGTGTGCTTTCAGAAAGCTCCACCTAGTGTGTTGAAAACCTCTGTGGAAGATATC | 900 |
| QY | 901 | TAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAAGCCCATCAGTCAGACA | 960 |
| Db | 901 | TAAGCAAGAAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAAGCCCATCAGTCAGACA | 960 |
| QY | 961 | CAGAGACGCTGCGGCTCGGCTCGCATGTCAACACCGAGTACGTGGGCCCCAGCTCGGAGA | 1020 |
| Db | 961 | CAGAGACGCTGCGGCTCGGCTCGCATGTCAACACCGAGTACGTGGGCCCCAGCTCGGAGA | 1020 |
| QY | 1021 | GGAGGCCGAGGTGTGCGAAACGCTCGCGAGGAGCTGGGAAACATGTCAGAGAGCTCT | 1080 |
| Db | 1021 | GGAGGCCGAGGTGTGCGAAACGCTCGCGAGGAGCTGGGAAACATGTCAGAGAGCTCT | 1080 |
| QY | 1081 | CGGGCTTCCAGCTCTCGTGAACAGCTCAGCGAGAACCTCAAGAGAGTGTGGAATGATA | 1140 |
| Db | 1081 | CGGGCTTCCAGCTCTCGTGAACAGCTCAGCGAGAACCTCAAGAGAGTGTGGAATGATA | 1140 |
| QY | 1141 | ACCAGTTTCTTGGGAGCTCATTTGCTGGCCCTCTCTAAGACAAGGAACATGTCAGCTTGT | 1200 |
| Db | 1141 | ACCAGTTTCTTGGGAGCTCATTTGCTGGCCCTCTCTAAGACAAGGAACATGTCAGCTTGT | 1200 |
| QY | 1201 | GGCAGGATGCGCGGCTCTTTTTCGCGAAATGAACGTGGGTGGTGGACAGCTGCACACGT | 1260 |
| Db | 1201 | GGCAGGATGCGCGGCTCTTTTTCGCGAAATGAACGTGGGTGGTGGACAGCTGCACACGT | 1260 |
| QY | 1261 | GTACCTTCAAGAAATTTAAACACATTTGCCACCAATTCACCTGCCCGCTGCACACCTTGG | 1320 |
| Db | 1261 | GTACCTTCAAGAAATTTAAACACATTTGCCACCAATTCACCTGCCCGCTGCACACCTTGG | 1320 |
| QY | 1321 | CCAGTCCATCTTGTGTAAGGCGAATGCTGCGCTTCTGCTCCACTCGGTGACGCGTG | 1380 |
| Db | 1321 | CCAGTCCATCTTGTGTAAGGCGAATGCTGCGCTTCTGCTCCACTCGGTGACGCGTG | 1380 |
| QY | 1381 | AGGAGGCTTGGTCTCGTGGGAGAGTGGACCCAGTCTCGGTGACGTGTGGCTCTGSGA | 1440 |
| Db | 1381 | AGGAGGCTTGGTCTCGTGGGAGAGTGGACCCAGTCTCGGTGACGTGTGGCTCTGSGA | 1440 |
| QY | 1441 | CCAGCAGAGAGGCGGCTCTGTGACGTCCACAGACACCTGCTTGGGGCCCTCGATCC | 1500 |
| Db | 1441 | CCAGCAGAGAGGCGGCTCTGTGACGTCCACAGACACCTGCTTGGGGCCCTCGATCC | 1500 |
| QY | 1501 | AGCACGGCTTGCAGTCTGAGCAAGTGTACACCCGATCCCGCAGAGACGCGGCTGGA | 1560 |
| Db | 1501 | AGCACGGCTTGCAGTCTGAGCAAGTGTACACCCGATCCCGCAGAGACGCGGCTGGA | 1560 |
| QY | 1561 | GCCACTGGTCACTTGGTCTTTCATGCTCTGTGACCTGTGGAGTTGGCAATATCACAGCA | 1620 |
| Db | 1561 | GCCACTGGTCACTTGGTCTTTCATGCTCTGTGACCTGTGGAGTTGGCAATATCACAGCA | 1620 |
| QY | 1621 | TCCGCTCTGCAACTCCCACTGCTGACGTGGGGGCAAGATTCGCAAGGAGTGGCC | 1680 |
| Db | 1621 | TCCGCTCTGCAACTCCCACTGCTGACGTGGGGGCAAGATTCGCAAGGAGTGGCC | 1680 |
| QY | 1681 | GGGAGACCAAGCCTGCCAGGCGCCCATGCCCCAATCGATGGCGCTGGAGCCCTGGT | 1740 |
| Db | 1681 | GGGAGACCAAGCCTGCCAGGCGCCCATGCCCCAATCGATGGCGCTGGAGCCCTGGT | 1740 |
| QY | 1741 | CCCCGTGGTGGCTGCACTGTCACTTGTGCGGTGGGATCCGGGAGCGCACCCGGGTCT | 1800 |
| Db | 1741 | CCCCGTGGTGGCTGCACTGTCACTTGTGCGGTGGGATCCGGGAGCGCACCCGGGTCT | 1800 |
| QY | 1801 | GCAACAGCCTGAGCCTCAGTACGGAGGAGAGGCGCTGGTGGGGATGTGCAAGAGCGTC | 1860 |
| Db | 1801 | GCAACAGCCTGAGCCTCAGTACGGAGGAGAGGCGCTGGTGGGGATGTGCAAGAGCGTC | 1860 |
| QY | 1861 | AGATGTGCAACAAGAGGAGCTGCGGCTGGATGCTGTTTATCCACCCCTGCTCCCG | 1920 |
| Db | 1861 | AGATGTGCAACAAGAGGAGCTGCGGCTGGATGCTGTTTATCCACCCCTGCTCCCG | 1920 |

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|----------------------------|--|---|--------------------|
| Db | 5161 | TTTTTTTGGCTTAAAGTTAGTCATGATCTCTTTCTGCGAGGAAATAGTCATCTATCCACATCCACAT | 5222 |
| Qy | 5221 | AAGGGGTTTATAGTAAGAAAGTCTGCTGCTCTGATGATGGATAGGGGGCAAAATCTTTTTTCC | 5280 |
| Db | 5221 | AAGGGGTTTATAGTAAGAAAGTCTGCTGCTCTGATGATGGATAGGGGGCAAAATCTTTTTTCC | 5280 |
| Qy | 5281 | CTTTTCTGTTTAATAGTCATCACATTTCTATGCGAACAGAAACGATCCATAACTTTAGTC | 5340 |
| Db | 5281 | CTTTTCTGTTTAATAGTCATCACATTTCTATGCGAACAGAAACGATCCATAACTTTAGTC | 5340 |
| Qy | 5341 | TTAATGTCACACATTTGGATTTGATAAAATTAATTTGTTGTTTCCCTTTGAGGTGATCGT | 5400 |
| Db | 5341 | TTAATGTCACACATTTGGATTTGATAAAATTAATTTGTTGTTTCCCTTTGAGGTGATCGT | 5400 |
| Qy | 5401 | TGTTGTTTTTGTGTCACATTTTTTACATTTTTTTCGCTGTGGAGCTGTATTCCCGAGACAACG | 5460 |
| Db | 5401 | TGTTGTTTTTGTGTCACATTTTTTACATTTTTTTCGCTGTGGAGCTGTATTCCCGAGACAACG | 5460 |
| Qy | 5461 | AAGCGTTGGGATACCTCAATTAATGTAAGCACTGTCAACAGCGTCGACGTTTCTGTTTC | 5520 |
| Db | 5461 | AAGCGTTGGGATACCTCAATTAATGTAAGCACTGTCAACAGCGTCGACGTTTCTGTTTC | 5520 |
| Qy | 5521 | TGCTCTGTGGGGTCAACCGTACAAATGCTGTGGGAATGACGATGATGTGAATATTAGAAAT | 5580 |
| Db | 5521 | TGCTCTGTGGGGTCAACCGTACAAATGCTGTGGGAATGACGATGATGTGAATATTAGAAAT | 5580 |
| Qy | 5581 | GTACCATATTTTTGTAAATTAATTTATGTTTTCTTAAACAAATTTATCGTATAGGTTGAT | 5640 |
| Db | 5581 | GTACCATATTTTTGTAAATTAATTTATGTTTTCTTAAACAAATTTATCGTATAGGTTGAT | 5640 |
| Qy | 5641 | GAACGTCATGTGTTTGGCCAAAGACTGTAAATATTTATTTATGTTGCACATGGTCAAA | 5700 |
| Db | 5641 | GAACGTCATGTGTTTGGCCAAAGACTGTAAATATTTATTTATGTTGCACATGGTCAAA | 5700 |
| Qy | 5701 | ATTTCCACCTGAAACCGTCGACTTAGCTAGAACCTCATTTTTTAAAGATTAAACACAGGA | 5760 |
| Db | 5701 | ATTTCCACCTGAAACCGTCGACTTAGCTAGAACCTCATTTTTTAAAGATTAAACACAGGA | 5760 |
| Qy | 5761 | AATAAATGTAATAAAGGTTTTCT 5784 | |
| Db | 5761 | AATAAATGTAATAAAGGTTTTCT 5784 | |
| RESULT | 3 | | |
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| DEFINITION | Sequence 2160 from Patent WO0229103. | | |
| ACCESSION | AX409513 | | |
| VERSION | AX409513.1 | GI:21442218 | |
| KEYWORDS | human. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| AUTHORS | Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G. | | |
| TITLE | Gene expression profiles in liver cancer | | |
| JOURNAL | Patent: WO 0229103-A 2160 11-APR-2002; | | |
| FEATURES | GENE LOGIC INC (US) | | |
| source | Location/Qualifiers | | |
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| | /organism="Homo sapiens" | | |
| | /db_xref="taxon:9606" | | |
| | /note="ENBL/GenBank Accession No. L12350" | | |
| BASE COUNT | 1447 a 1460 c 1518 g 1359 t | | |
| ORIGIN | | | |
| Query Match | 100.0%; | Score 5784; | DB 6; Length 5784; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | |
| Matches 5784; Conservative | 0; | Mismatches | 0; Indels 0; Gaps |
| Qy | 1 | ACGGCATCCAGTACAGAGGGCTGGACTTTGGACCCCTGCAGCAGCCCTGCACAGGAGAAG | 60 |

Db 1 ACGGCATCCAGTACAGAGGGCTGGACTTTGAGCCCTGCAGCAGCCCTGCACAGGAGAG 60
Qy 61 CGGCATATAAGCCGCTGCGCGGAGCCGCTCGGCCACCTCCACCGAGCATCTCTGCA 120
Db 61 CGGCATATAAGCCGCTGCGCGGAGCCGCTCGGCCACCTCCACCGAGCATCTCTGCA 120
Qy 121 CTGCAGGCGCGTCTCTGCTCCAGCAGAGCCTGGCCCTTTCTGACTCGGTCCGGAAAC 180
Db 121 CTGCAGGCGCGTCTCTGCTCCAGCAGAGCCTGGCCCTTTCTGACTCGGTCCGGAAAC 180
Qy 181 TGAACACAGTCACTCATCTCTTTTGGCAAAACAGGAGCTCAGCTCAGGAGCAGGA 240
Db 181 TGAACACAGTCACTCATCTCTTTTGGCAAAACAGGAGCTCAGCTCAGGAGCAGGA 240
Qy 241 TGGTCTGAGGCTGGTCTGCTGCTGTGGTGTGGCCCGAGCACGCAAGCTGTGTACC 300
Db 241 TGGTCTGAGGCTGGTCTGCTGCTGTGGTGTGGCCCGAGCACGCAAGCTGTGTACC 300
Qy 301 AGGACAAAGACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGACCAT 360
Db 301 AGGACAAAGACAGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGACCAT 360
Qy 361 CGGCAAGCAGTTCGCGGGGCCGACCCGCTGCGGGCTTACCGCTTCGTGCGCTTTG 420
Db 361 CGGCAAGCAGTTCGCGGGGCCGACCCGCTGCGGGCTTACCGCTTCGTGCGCTTTG 420
Qy 421 ACTACATCCCAACCGGTGAACAGATGACCTCAGCAAGATCACCAGATCATCGGCAGA 480
Db 421 ACTACATCCCAACCGGTGAACAGATGACCTCAGCAAGATCACCAGATCATCGGCAGA 480
Qy 481 AGGAGGCTTCTTCTCAGCGCCAGCTCAAGCAGGAGCGGAAGTCCAGGGCAGCTGT 540
Db 481 AGGAGGCTTCTTCTCAGCGCCAGCTCAAGCAGGAGCGGAAGTCCAGGGCAGCTGT 540
Qy 541 TGGCTCTGGAGGGCCCGGCTCTCTCCAGAGGCAGTTTCAGATCGTCTCCAAACGCCCC 600
Db 541 TGGCTCTGGAGGGCCCGGCTCTCTCCAGAGGCAGTTTCAGATCGTCTCCAAACGCCCC 600
Qy 601 CGGACAGCTGGATCTCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 660
Db 601 CGGACAGCTGGATCTCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 660
Qy 661 ACCTCGGCTTGGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 720
Db 661 ACCTCGGCTTGGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 720
Qy 721 ACAGCTTGACGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 780
Db 721 ACAGCTTGACGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 780
Qy 781 AGCAGCTGAGGCGGAAAGAGCGGATGTACGTGGCCAAAGGCTCTGCCAGAGAGTC 840
Db 781 AGCAGCTGAGGCGGAAAGAGCGGATGTACGTGGCCAAAGGCTCTGCCAGAGAGTC 840
Qy 841 ACTTCAGGGTTTCTTCAGAACGCTTCACTTACCTTACCTTACCTTACCTTACCTTAC 900
Db 841 ACTTCAGGGTTTCTTCAGAACGCTTCACTTACCTTACCTTACCTTACCTTACCTTAC 900
Qy 901 TAAGCAAGAGGTTTGCAGCAAGGCGGAGCTGAGATCAAGCCATCAGTGAGAAC 960
Db 901 TAAGCAAGAGGTTTGCAGCAAGGCGGAGCTGAGATCAAGCCATCAGTGAGAAC 960
Qy 961 CAGAGAGCTGCGGCTGGGTCGGATGTACACCGAGTACGTGGGCGCCAGCTTCGAGA 1020
Db 961 CAGAGAGCTGCGGCTGGGTCGGATGTACACCGAGTACGTGGGCGCCAGCTTCGAGA 1020
Qy 1021 GGAGGCGGAGGTTGCGAACGCTTCGCGAGGAGCTGGGAAACATGGTCAGAGCTCT 1080
Db 1021 GGAGGCGGAGGTTGCGAACGCTTCGCGAGGAGCTGGGAAACATGGTCAGAGCTCT 1080
Qy 1081 CGGGGCTCCAGCTCTCGTGAACAGCTCAGCAGAGACCTCAAGAGAGTGTGGAATGATA 1140
Db 1081 CGGGGCTCCAGCTCTCGTGAACAGCTCAGCAGAGACCTCAAGAGAGTGTGGAATGATA 1140

Qy 1141 ACCAGTTTCTCTGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACATGTCACTTGT 1200
Db 1141 ACCAGTTTCTCTGGAGCTCATTTGGTGGCCCTCTTAAGACAAGGAACATGTCACTTGT 1200
Qy 1201 GGCAGGATGGCGGTTCTTTTCGGGAAATGAACGTGGGTGGTGCAGCTGCACACAGT 1260
Db 1201 GGCAGGATGGCGGTTCTTTTCGGGAAATGAACGTGGGTGGTGCAGCTGCACACAGT 1260
Qy 1261 GTACTCTCAAGAAATTTAAACCAATTTGCCACCAATCACCCTGCCCTGCAACCTCGG 1320
Db 1261 GTACTCTCAAGAAATTTAAACCAATTTGCCACCAATCACCCTGCCCTGCAACCTCGG 1320
Qy 1321 CCAGTCCATCCTTTTGTGAAGGCGAATGCTGCCCTTCCCTGCTCCACTCGGTGGACGG 1380
Db 1321 CCAGTCCATCCTTTTGTGAAGGCGAATGCTGCCCTTCCCTGCTCCACTCGGTGGACGG 1380
Qy 1381 AGGAGGCTGTCTCCGTGGGCGAGTGGAGCCAGTGTCTCCGTCCACTCGGTGGACGG 1440
Db 1381 AGGAGGCTGTCTCCGTGGGCGAGTGGAGCCAGTGTCTCCGTCCACTCGGTGGACGG 1440
Qy 1441 CCCAGCAGAGGCGGCTCTGTGACGTCACCCGCGCATCCGGCAGACCGCGGCTGGA 1500
Db 1441 CCCAGCAGAGGCGGCTCTGTGACGTCACCCGCGCATCCGGCAGACCGCGGCTGGA 1500
Qy 1501 AGACACGGGCTTGAGTGTGAGCAAGTGTGACACCCGCGCATCCGGCAGACCGCGGCTGGA 1560
Db 1501 AGACACGGGCTTGAGTGTGAGCAAGTGTGACACCCGCGCATCCGGCAGACCGCGGCTGGA 1560
Qy 1561 GCCACTGGTCACTTGGTCTTCATGCTGTGACCTGTGGAGTTGGCAATATCACAGCA 1620
Db 1561 GCCACTGGTCACTTGGTCTTCATGCTGTGACCTGTGGAGTTGGCAATATCACAGCA 1620
Qy 1621 TCCGCTCTGCAACTCCCGAGTGGCGGAGGAGGCTGTGAGTGGCGCTTGGAGGAGTGCC 1680
Db 1621 TCCGCTCTGCAACTCCCGAGTGGCGGAGGAGGCTGTGAGTGGCGCTTGGAGGAGTGCC 1680
Qy 1681 GGGAGACAAAGCCTGCGAGGCGCCCATGATGCCCAATCGATGGCGCTTGGAGGAGTGCC 1740
Db 1681 GGGAGACAAAGCCTGCGAGGCGCCCATGATGCCCAATCGATGGCGCTTGGAGGAGTGCC 1740
Qy 1741 CCCCGTGGTGGGCTTGCACCTGTACCTGTGCGGCTGGGATCCCGGAGCGCACCGGCT 1800
Db 1741 CCCCGTGGTGGGCTTGCACCTGTACCTGTGCGGCTGGGATCCCGGAGCGCACCGGCT 1800
Qy 1801 GCAACAGCCTGAGCCTCAGTACGAGGAGGAGGCTGTGCGGGGAGTGTGAGGAGGCTC 1860
Db 1801 GCAACAGCCTGAGCCTCAGTACGAGGAGGAGGCTGTGCGGGGAGTGTGAGGAGGCTC 1860
Qy 1861 AGATGTCAACAAGAGAGCTGCCCGTGGATGGCTGTATCCAAACCCCTGTCCCGG 1920
Db 1861 AGATGTCAACAAGAGAGCTGCCCGTGGATGGCTGTATCCAAACCCCTGTCCCGG 1920
Qy 1921 GAGCCAGTGCAGCAGCTTCCCGATGGTCTGTGATGGGCTTTCGCCCTGTGGGCT 1980
Db 1921 GAGCCAGTGCAGCAGCTTCCCGATGGTCTGTGATGGGCTTTCGCCCTGTGGGCT 1980
Qy 1981 TCTTGGCAATGGCAGCCTGTGAGGAGCTTGGAGGAGTGTGCGGCTGTCCCGACATCT 2040
Db 1981 TCTTGGCAATGGCAGCCTGTGAGGAGCTTGGAGGAGTGTGCGGCTGTCCCGACATCT 2040
Qy 2041 GCTTCTCCACAGCAAGTGCCTGTGTGTCAACACTCAGCCTTGGCTTCCACTGCTGC 2100
Db 2041 GCTTCTCCACAGCAAGTGCCTGTGTGTCAACACTCAGCCTTGGCTTCCACTGCTGC 2100
Qy 2101 CTTGCCCGCCCGGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Db 2101 CTTGCCCGCCCGGATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Qy 2161 CGGAAAAGCAAGTGTGTGAGCGGAAACCCATGCAAGGAGCAAGACACAACTGCCACA 2220
Db 2161 CGGAAAAGCAAGTGTGTGAGCGGAAACCCATGCAAGGAGCAAGACACAACTGCCACA 2220

| | | | |
|----|------|---|------|
| Qy | 2221 | AGCAGCGGAGTGCATCTACCTGGGTGTCATCTCAGGACCCCATATGTACAAGTGCAGGTGCC | 2280 |
| Db | 2221 | AGCAGCGGAGTGCATCTACCTGGGTGTCATCTCAGGACCCCATATGTACAAGTGCAGGTGCC | 2280 |
| Qy | 2281 | AGCAGGCTACGCGGGCGAGGGGCTCATCTCGGGGAGGACTCGGACCTGGACGGCTGCC | 2340 |
| Db | 2281 | AGCAGGCTACGCGGGCGAGGGGCTCATCTCGGGGAGGACTCGGACCTGGACGGGCTGCC | 2340 |
| Qy | 2341 | CCAACTCTCAATCTGGTCTGGCCACCAACGCCACCTACCACTGCATCAAGGATAACTGCC | 2400 |
| Db | 2341 | CCAACTCTCAATCTGGTCTGGCCACCAACGCCACCTACCACTGCATCAAGGATAACTGCC | 2400 |
| Qy | 2401 | CCCATCTGCCAAATCTCGGCGAGGAAGACTTTGACAAGGAGGGATTGGCATGCCGTGTG | 2460 |
| Db | 2401 | CCCATCTGCCAAATCTCGGCGAGGAAGACTTTGACAAGGAGGGATTGGCATGCCGTGTG | 2460 |
| Qy | 2461 | ATGATGACGATGACAATGACGGTGTGACCGATGACAGGACAACTGCCAGCTCCCTCTCA | 2520 |
| Db | 2461 | ATGATGACGATGACAATGACGGTGTGACCGATGACAGGACAACTGCCAGCTCCCTCTCA | 2520 |
| Qy | 2521 | ATCCCCGCCAGGCTGACTATGACAAGGATGAGGTTGGGACCGCTGTGACAACCTGCCCTT | 2580 |
| Db | 2521 | ATCCCCGCCAGGCTGACTATGACAAGGATGAGTGGTGGGACCGCTGTGACAACCTGCCCTT | 2580 |
| Qy | 2581 | ACGTGCAACAACCTGCCAGATCGACACAGACAACAATGGAGAGGGTGACGCTGCTCCG | 2640 |
| Db | 2581 | ACGTGCAACAACCTGCCAGATCGACACAGACAACAATGGAGAGGGTGACGCTGCTCCG | 2640 |
| Qy | 2641 | TGGACATTTGATGGGACGATGCTTCAATGACAGAGACAATTTGCCCTACGCTCTACAACA | 2700 |
| Db | 2641 | TGGACATTTGATGGGACGATGCTTCAATGACAGAGACAATTTGCCCTACGCTCTACAACA | 2700 |
| Qy | 2701 | CTGACCAAGGGACACGGATGGTGACGGTGTGGGGATCACTGTGACAACCTGCCCTCG | 2760 |
| Db | 2701 | CTGACCAAGGGACACGGATGGTGACGGTGTGGGGATCACTGTGACAACCTGCCCTCG | 2760 |
| Qy | 2761 | TGCACAACCTGTACCAAGACGGAGTGGACAATGACCTTTGGGGACACAGTGTGACAACA | 2820 |
| Db | 2761 | TGCACAACCTGTACCAAGACGGAGTGGACAATGACCTTTGGGGACACAGTGTGACAACA | 2820 |
| Qy | 2821 | ACGAGGACATAGATGACGACGGCCACCAAGACAACACGAGACAACCTGCCCTACATCTCCA | 2880 |
| Db | 2821 | ACGAGGACATAGATGACGACGGCCACCAAGACAACACGAGACAACCTGCCCTACATCTCCA | 2880 |
| Qy | 2881 | ACGCCAACCAAGCTGACCATGTACAGACAGCGCCAGGGCGACGCTGTGACCTCATGATG | 2940 |
| Db | 2881 | ACGCCAACCAAGCTGACCATGTACAGACAGCGCCAGGGCGACGCTGTGACCTCATGATG | 2940 |
| Qy | 2941 | ACAACGATGGCGTCCCGATGACAGGGACAACCTGCCGGCTGTGTTCAACCCAGACCCAGG | 3000 |
| Db | 2941 | ACAACGATGGCGTCCCGATGACAGGGACAACCTGCCGGCTGTGTTCAACCCAGACCCAGG | 3000 |
| Qy | 3001 | AGGACTTGGACGGTGTGACGGGGTGATTTTGTAAAGATGATTTTGACAATGACAACA | 3060 |
| Db | 3001 | AGGACTTGGACGGTGTGACGGGGTGATTTTGTAAAGATGATTTTGACAATGACAACA | 3060 |
| Qy | 3061 | TCCCAGATATTGATGTGTGCTCTGAAAACAATGCCATCAGTGAGACAGACTTCAGGA | 3120 |
| Db | 3061 | TCCCAGATATTGATGTGTGCTCTGAAAACAATGCCATCAGTGAGACAGACTTCAGGA | 3120 |
| Qy | 3121 | ACTTCCAGATGTGCCCTTGGATTCGCAAGGACCAACCCAAATGATCCCAACTGGGTCA | 3180 |
| Db | 3121 | ACTTCCAGATGTGCCCTTGGATTCGCAAGGACCAACCCAAATGATCCCAACTGGGTCA | 3180 |
| Qy | 3181 | TTGCCCATCAAGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCGGGATCCCTGTAG | 3240 |
| Db | 3181 | TTGCCCATCAAGCAAGGAGCTGGTTCAGACAGCCAACTCGGACCCCGGGATCCCTGTAG | 3240 |
| Qy | 3241 | GTTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGGCACATTTCTAGCTAAACACTCACCGGG | 3300 |
| Db | 3241 | GTTTTTGACGAGTTTGGGTCTGTGGACTTCAGTGGGCACATTTCTAGCTAAACACTCACCGGG | 3300 |
| Qy | 3301 | ACGACGACTATGCTGGCTTCGCTTTTGGTTTACCAGTCAAGCAGCGGCTCTATGTGGTGA | 3360 |

| | | | |
|----|------|--|------|
| Db | 3301 | ACGACGACTATGCTGGCTTGGCTTGGGTTACAGTCAAGCAGCGCTTCTATGTGGTGA | 3360 |
| Qy | 3361 | TGTGGAAGCAGGTGACGACAGCACTACTGGAGAGACCCAGCGGCGCTATGCTACT | 3420 |
| Db | 3361 | TGTGGAAGCAGGTGACGACAGCACTACTGGAGAGACCCAGCGGCGCTATGCTACT | 3420 |
| Qy | 3421 | CCGGCGTGTCCCTCAAGTGGTGAACCTCCACCAGGGAGCGGCGAGCACTGAGGAACG | 3480 |
| Db | 3421 | CCGGCGTGTCCCTCAAGTGGTGAACCTCCACCAGGGAGCGGCGAGCACTGAGGAACG | 3480 |
| Qy | 3481 | CGCTGTGGCACACGGGGAACACGCCGGGCGAGTGGGAACCTTTATGGCACGCCACCGA | 3540 |
| Db | 3481 | CGCTGTGGCACACGGGGAACACGCCGGGCGAGTGGGAACCTTTATGGCACGCCACCGA | 3540 |
| Qy | 3541 | ACATTGGCTGGAAGGACTCACCGGCTATAGTGGCACTGACTCACAGGCCCAAGACCG | 3600 |
| Db | 3541 | ACATTGGCTGGAAGGACTCACCGGCTATAGTGGCACTGACTCACAGGCCCAAGACCG | 3600 |
| Qy | 3601 | GCTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTCAATGGCAGACTCAGGACCTATCT | 3660 |
| Db | 3601 | GCTACATCAGAGTCTTAGTGCATGAAGGAAACAGGTCAATGGCAGACTCAGGACCTATCT | 3660 |
| Qy | 3661 | ATGACCAAACCTAGCTGGCGGGCGGTGGGTCTATTGTCTCTCTCAAGAAATGGTCT | 3720 |
| Db | 3661 | ATGACCAAACCTAGCTGGCGGGCGGTGGGTCTATTGTCTCTCTCAAGAAATGGTCT | 3720 |
| Qy | 3721 | ATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTGCTGCATTTCCG | 3780 |
| Db | 3721 | ATTTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTGCTGCATTTCCG | 3780 |
| Qy | 3781 | CAATGCCCTGTGATGCCATGGTCCCTAGACACCTCAGTTCATTTGTGTCCTTGGCGGT | 3840 |
| Db | 3781 | CAATGCCCTGTGATGCCATGGTCCCTAGACACCTCAGTTCATTTGTGTCCTTGGCGGT | 3840 |
| Qy | 3841 | CTCTCTCTAGAGACCTCCTGCTCCCTTACCTTTAACTCTGATGGTCTTCACTCCTCCTGC | 3900 |
| Db | 3841 | CTCTCTCTAGAGACCTCCTGCTCCCTTACCTTTAACTCTGATGGTCTTCACTCCTCCTGC | 3900 |
| Qy | 3901 | CAGCAACCCCAACCCCAAGTGCCCTCAGAGGATAAATATCAATGAACCTCAGAGATGAAC | 3960 |
| Db | 3901 | CAGCAACCCCAACCCCAAGTGCCCTCAGAGGATAAATATCAATGAACCTCAGAGATGAAC | 3960 |
| Qy | 3961 | ATCTAACCCCACTAGAGAAACCAAGTTGGTGATATAGACTTTTATGTGGAGTGAAT | 4020 |
| Db | 3961 | ATCTAACCCCACTAGAGAAACCAAGTTGGTGATATAGACTTTTATGTGGAGTGAAT | 4020 |
| Qy | 4021 | TGGGCATGCCATTACATPGCTTTTCTGTTGTTTAAAAAGAAATGACGTTTACATATA | 4080 |
| Db | 4021 | TGGGCATGCCATTACATPGCTTTTCTGTTGTTTAAAAAGAAATGACGTTTACATATA | 4080 |
| Qy | 4081 | AATCTAATTACTTATTTCTATTTATGCTATATGGAGTTGAAAGGAAATACTGTGCATAGC | 4140 |
| Db | 4081 | AATCTAATTACTTATTTCTATTTATGCTATATGGAGTTGAAAGGAAATACTGTGCATAGC | 4140 |
| Qy | 4141 | CATTATGATAAATTAAGCATGAATAATTTGCTGAACTACTTTTGGTGCTTAAAGTTGTC | 4200 |
| Db | 4141 | CATTATGATAAATTAAGCATGAATAATTTGCTGAACTACTTTTGGTGCTTAAAGTTGTC | 4200 |
| Qy | 4201 | ACTATTCTTGAATFAGAGTTGCTCTACAATGACACACAAATCCCCTCAATAAATATATA | 4260 |
| Db | 4201 | ACTATTCTTGAATFAGAGTTGCTCTACAATGACACACAAATCCCCTCAATAAATATATA | 4260 |
| Qy | 4261 | ACAAGGTCAATTCAAATTTGAAGTAAATGTTTTAGTAAAGGAGATTTAGAAGACAACAGG | 4320 |
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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AUTHORS McCarthy J.
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prevention and therapy of cardiovascular disease
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1 (bases 1 to 5784)
LaBell,T.L., Milewicz,D.J., Distèche,C.M. and Byers,P.H.
Thrombospondin II: partial cDNA sequence, chromosome location, and
expression of a second member of the thrombospondin gene family in
humans
Genomics 12 (3), 421-429 (1992)
92217961
1559694
2 (bases 1 to 5784)
LaBell,T.L. and Byers,P.H.
Sequence and characterization of the complete human thrombospondin
2 cDNA: potential regulatory role for the 3' untranslated region
Genomics 17 (1), 225-229 (1993)
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| Qy | 181 TGAACACGATCATCATGTCATCTTTTGGCAAAACAGGAGCTCAGCTCGAGGAGCAGA 240 |
| Db | 181 TGAACACGATCATCATGTCATCTTTTGGCAAAACAGGAGCTCAGCTCGAGGAGCAGA 240 |
| Qy | 241 TGGTCTGGAGGCTGGTCCCTGCTGGCTCTGTGGGTGTGGCCAGCACGCAAGCTGCTACC 300 |
| Db | 241 TGGTCTGGAGGCTGGTCCCTGCTGGCTCTGTGGGTGTGGCCAGCACGCAAGCTGCTACC 300 |
| Qy | 301 AGGACAAGACACAGCCTTCAGCTTTTCAGTATCAGCAACATCAACCGCAAGACATTG 360 |
| Db | 301 AGGACAAGACACAGCCTTCAGCTTTTCAGTATCAGCAACATCAACCGCAAGACATTG 360 |
| Qy | 361 CGGCAAGACGTCCTCGGGGGCCGACCCGCTGCGGGCTTACCGCTTCGTGCGCTTTG 420 |
| Db | 361 CGGCAAGACGTCCTCGGGGGCCGACCCGCTGCGGGCTTACCGCTTCGTGCGCTTTG 420 |
| Qy | 421 ACTACATCCCACCGGTGAACGAGATGACCTCAGCAAGATCACCAGATCATCGGCAGA 480 |
| Db | 421 ACTACATCCCACCGGTGAACGAGATGACCTCAGCAAGATCACCAGATCATCGGCAGA 480 |
| Qy | 481 AGGAGGGCTTCTCCTCAGCGGCCAGCTCAAGCAGGAGCGCAAGTCCAGGGCAGCGTGT 540 |
| Db | 481 AGGAGGGCTTCTCCTCAGCGGCCAGCTCAAGCAGGAGCGCAAGTCCAGGGCAGCGTGT 540 |
| Qy | 541 TGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGCGAGTTCAGATCGTCTCCAACGGCCCCG 600 |
| Db | 541 TGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGCGAGTTCAGATCGTCTCCAACGGCCCCG 600 |
| Qy | 601 CGGACAGCTGGATCTCACCTACTCTGGAATGACGGCACCCCGCATGTGGTCTCCCTGGAGG 660 |
| Db | 601 CGGACAGCTGGATCTCACCTACTCTGGAATGACGGCACCCCGCATGTGGTCTCCCTGGAGG 660 |
| Qy | 661 ACGTGCGCCTGGCTGACTTCGCGAGTGGAGAACGTCACCGTTCAGGTGGCTGGCGAGACCT 720 |
| | |

| | | | |
|----|------|---|------|
| Qy | 1801 | GCAACAGCCCTGAGCCCTCACTAGTACGGAGGAAAGCCCTGCTGGGGGATGTGCAGGAGGCTC | 1861 |
| Db | 1801 | GCAACAGCCCTGAGCCCTCACTAGTACGGAGGAAAGCCCTGCTGGGGATGTGCAGGAGGCTC | 1860 |
| Qy | 1861 | AGATGTGCAACACAGAGAGCTGCCCGTGGATGGCTGTTTATCCAAACCCCTGCTTCCCGG | 1920 |
| Db | 1861 | AGATGTGCAACACAGAGAGCTGCCCGTGGATGGCTGTTTATCCAAACCCCTGCTTCCCGG | 1920 |
| Qy | 1921 | GAGCCCAAGTCACAGACTTCCCGGATGGGTCTGTGTCATGCGGCTTTCGCCCTGTGGGCT | 1980 |
| Db | 1921 | GAGCCCAAGTCACAGACTTCCCGGATGGGTCTGTGTCATGCGGCTTTCGCCCTGTGGGCT | 1980 |
| Qy | 1981 | TCTTGGGCAATGGCACCCACTGTGAGGACCTGGACGAGTGTGCCCTGGTCCCGACATCT | 2040 |
| Db | 1981 | TCTTGGGCAATGGCACCCACTGTGAGGACCTGGACGAGTGTGCCCTGGTCCCGACATCT | 2040 |
| Qy | 2041 | GCTTCTCCACAGAGGTGCCCTGCTGTGTGTCACACACTCAGCTTGGCTTCCACTGGCTGC | 2100 |
| Db | 2041 | GCTTCTCCACAGAGGTGCCCTGCTGTGTGTCACACACTCAGCTTGGCTTCCACTGGCTGC | 2100 |
| Qy | 2101 | CCTGCGCGCCCGCATACAGAGGAAACACGCGCTCGGGTGGCTTGAAGACGCAAGA | 2160 |
| Db | 2101 | CCTGCGCGCCCGCATACAGAGGAAACACGCGCTCGGGTGGCTTGAAGACGCAAGA | 2160 |
| Qy | 2161 | CGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGGACAAGACACACAACCTGCCACA | 2220 |
| Db | 2161 | CGGAAAAGCAAGTGTGTGAGCCCGAAAACCCATGCAAGGACAAGACACACAACCTGCCACA | 2220 |
| Qy | 2221 | AGCACGGGAGTGCATCTTACCTGGGTCACTTCAGCGACCCCATGTACAGTGCAGTGCC | 2280 |
| Db | 2221 | AGCACGGGAGTGCATCTTACCTGGGTCACTTCAGCGACCCCATGTACAGTGCAGTGCC | 2280 |
| Qy | 2281 | AGCAGCTACGCGGGCGGCGGCTCATCTCGGGGGAGGACTCGGACCTGGACGGCTGGC | 2340 |
| Db | 2281 | AGCAGGCTACGCGGGCGAGGGCTCATCTCGGGGGAGGACTCGGACCTGGACGGCTGGC | 2340 |
| Qy | 2341 | CCAACTCTAACTGTGCTGCGGCACCAACGCCACCTTACCCTTGCATCAAGGATAACTGCC | 2400 |
| Db | 2341 | CCAACTCTAACTGTGCTGCGGCACCAACGCCACCTTACCCTTGCATCAAGGATAACTGCC | 2400 |
| Qy | 2401 | CCCATCTGCCAAATCTTGGCGAGGAAAGACTTTGCAAGACGGGATGGCGATGCCTGTG | 2460 |
| Db | 2401 | CCCATCTGCCAAATCTTGGCGAGGAAAGACTTTGCAAGACGGGATTTGGCGATGCCTGTG | 2460 |
| Qy | 2461 | ATGATGACGATGACATGACGGTGTACCGATGCAAGACGAACTGCCAGCTCCTCTTCA | 2520 |
| Db | 2461 | ATGATGACGATGACATGACGGTGTACCGATGCAAGACGAACTGCCAGCTCCTCTTCA | 2520 |
| Qy | 2521 | ATCCCCGCCAGGCTGACTATGACAGGATGAGGTTGGGGACCGCTGTGACAACTGCCCTT | 2580 |
| Db | 2521 | ATCCCCGCCAGGCTGACTATGACAGGATGAGGTTGGGGACCGCTGTGACAACTGCCCTT | 2580 |
| Qy | 2581 | ACGTGCAACACCTGCCAGATCGACACAGACAACAATGGAGAGGTTGACGCTGCTCCG | 2640 |
| Db | 2581 | ACGTGCAACACACCTGCCAGATCGACACAGACAACAATGGAGAGGTTGACGCTGCTCCG | 2640 |
| Qy | 2641 | TGGACATTTGATGGGACGATGCTTCATGACGAGACAATTTGCCCTACGCTTACAACA | 2700 |
| Db | 2641 | TGGACATTTGATGGGACGATGCTTCATGACGAGACAATTTGCCCTACGCTTACAACA | 2700 |
| Qy | 2701 | CTGACCAGAGGACACGGATGTGTACGGTGTGGGGATCACTGTGACAACTGCCCCCTGG | 2760 |
| Db | 2701 | CTGACCAGAGGACACGGATGTGTACGGTGTGGGGATCACTGTGACAACTGCCCCCTGG | 2760 |
| Qy | 2761 | TGCACAACCTTGACAGACCGAGCTGGACAATGACCTTTGTTGGGACCAAGTGTGACAACA | 2820 |
| Db | 2761 | TGCACAACCTTGACAGACCGAGCTGGACAATGACCTTTGTTGGGACCAAGTGTGACAACA | 2820 |
| Qy | 2821 | ACGAGGACATAGATGACGAGGGCCACGACAACACGAGACAACCTGCCCTTACATCTCCA | 2880 |
| Db | 2821 | ACGAGGACATAGATGACGAGGGCCACGACAACACGAGACAACCTGCCCTTACATCTCCA | 2880 |

| | | | |
|----|------|--|------|
| QY | 2881 | ACGCCAACCCAGGCTGACCATGACAGAGACGGCCAGGGCGACCCCTGTGACCCCTGATGATG | 2940 |
| DB | 2881 | ACGCCAACCCAGGCTGACCATGACAGAGACGGCCAGGGCGACCCCTGTGACCCCTGATGATG | 2940 |
| QY | 2941 | ACACGATGGCGTCCCGATGACAGGACAACTGCCGGCTGTGTTCAACCCAGACACG | 3000 |
| DB | 2941 | ACACGATGGCGTCCCGATGACAGGACAACTGCCGGCTGTGTTCAACCCAGACACG | 3000 |
| QY | 3001 | AGGACTTGGACGGTGATGGACGGGTGATATTTGTAAGATGATTTTGACAATGACAACA | 3060 |
| DB | 3001 | AGGACTTGGACGGTGATGGACGGGTGATATTTGTAAGATGATTTTGACAATGACAACA | 3060 |
| QY | 3061 | TCCAGATATTGATGATGTGTCTGTAANAACATGCCATCAGTGAGACAGACTTCAGGA | 3120 |
| DB | 3061 | TCCAGATATTGATGATGTGTCTGTAANAACATGCCATCAGTGAGACAGACTTCAGGA | 3120 |
| QY | 3121 | ACTTCCAGATGGTCCCTCGATCCCAAAGGAGACCAACCAATTCATCCCACCTGGGTCA | 3180 |
| DB | 3121 | ACTTCCAGATGGTCCCTCGATCCCAAAGGAGACCAACCAATTCATCCCACCTGGGTCA | 3180 |
| QY | 3181 | TTCCGCCATCAAGGCAAGGAGCTGGTTTCAGACAGCCAACCTCGGACCCGGCATCGCTGTAG | 3240 |
| DB | 3181 | TTCCGCCATCAAGGCAAGGAGCTGGTTTCAGACAGCCAACCTCGGACCCGGCATCGCTGTAG | 3240 |
| QY | 3241 | GTTTGTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTTCTACGTAAACACTGACCGG | 3300 |
| DB | 3241 | GTTTGTGACGAGTTTGGGTCTGTGGACTTCAGTGGCACATTTCTACGTAAACACTGACCGG | 3300 |
| QY | 3301 | ACGACGACTATGCTGGGTCCTGCTTTTGGTTTACCAGTCAAGCAGCGCTTCTATGTGGTGA | 3360 |
| DB | 3301 | ACGACGACTATGCTGGGTCCTGCTTTTGGTTTACCAGTCAAGCAGCGCTTCTATGTGGTGA | 3360 |
| QY | 3361 | TGTTGGAAGCAGGTGACGCACACCTACTGGGAGGACCAAGCCACGGCGCTTATGGCTACT | 3420 |
| DB | 3361 | TGTTGGAAGCAGGTGACGCACACCTACTGGGAGGACCAAGCCACGGCGCTTATGGCTACT | 3420 |
| QY | 3421 | CCGGCGTGTCCCTCAAGGTGGTGAATCTCACACAGGGGAGCGGCGAGCACCTTGAGGAACG | 3480 |
| DB | 3421 | CCGGCGTGTCCCTCAAGGTGGTGAATCTCACACAGGGGAGCGGCGAGCACCTTGAGGAACG | 3480 |
| QY | 3481 | CGCTGTGGCACACGGGAAACACCCCGGGCGAGTGGCAACCTTATGGCAGCACCCACGGA | 3540 |
| DB | 3481 | CGCTGTGGCACACGGGAAACACCCCGGGCGAGTGGCAACCTTATGGCAGCACCCACGGA | 3540 |
| QY | 3541 | ACATTGGCTGGAAGGAGCTACACGGCTTATAGTGGCACCTGACTCACAGGGCCCAAGACCG | 3600 |
| DB | 3541 | ACATTGGCTGGAAGGAGCTACACGGCTTATAGTGGCACCTGACTCACAGGGCCCAAGACCG | 3600 |
| QY | 3601 | GCTACATCAGAGTCTTAGTGCATGAAGGAACACAGGTCAATGCGAGCTCAGSACCTATCT | 3660 |
| DB | 3601 | GCTACATCAGAGTCTTAGTGCATGAAGGAACACAGGTCAATGCGAGCTCAGSACCTATCT | 3660 |
| QY | 3661 | ATGACCAAACTACGCTGGCGGGCGTGGGTCTATTTCGTCTTCTCAAGAAATGGTCT | 3720 |
| DB | 3661 | ATGACCAAACTACGCTGGCGGGCGTGGGTCTATTTCGTCTTCTCAAGAAATGGTCT | 3720 |
| QY | 3721 | ATTTTCTCAGACCTCAAGTACGAATGACAGAGATTTTAAACAAGATTGCTGCATTTCCGG | 3780 |
| DB | 3721 | ATTTTCTCAGACCTCAAGTACGAATGACAGAGATTTTAAACAAGATTGCTGCATTTCCGG | 3780 |
| QY | 3781 | CAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCAATTTGGTTCCTTGGCGCTT | 3840 |
| DB | 3781 | CAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCAATTTGGTTCCTTGGCGCTT | 3840 |
| QY | 3841 | CTCTCTCAGACGACCTCTGTCCTTGGACCTTAACTCTGATGGTCTTTCACCTCCGTC | 3900 |
| DB | 3841 | CTCTCTCAGACGACCTCTGTCCTTGGACCTTAACTCTGATGGTCTTTCACCTCCGTC | 3900 |
| QY | 3901 | CAGAACCCCAAAACCCAAAGTGCCTTCAGAGGATAAATATCAATGCACTCAGAGATGAAC | 3960 |
| DB | 3901 | CAGAACCCCAAAACCCAAAGTGCCTTCAGAGGATAAATATCAATGCACTCAGAGATGAAC | 3960 |
| QY | 3961 | ATCTAACCCACTAGAGGAAACACAGTTTGGTGATATATGAGACTTTATGTGAGTGAAT | 4020 |

[illegible]

QY 1368 TCGGTGGACGGTTCAGAGAGGCTGCTCCGTGGCGAGAGTGCACCCAGTGCCTCGGTGAGG 1427
Db 1628 ----TGACGGAGAGAGGCTGGTCCCGTGGGGGAGTGCAGGAGTGCCTCAGCCAC 1682
QY 1428 TGTGGCTCTGGGACCCAGACAGAGAGCCGGTCTGTGAGCTCACCAGAACACCTGCTGTG 1487
Db 1683 TCGGGGTGGGACCCAGACAGAGCGGGCCGCTCCTGTGATGTCCACAGAACACCTGCTGTG 1742
QY 1488 GGGCCCTCGATCCAGACAGCGGCTTGCAGTCTGAGCAAGTGTGACACCCGCATCCGGCAG 1547
Db 1743 GGGCCGCTCATCCAGACAGCGGCTTGCAGCTTGGTCTTCACTGCTGTGACCTGTGGATTGGC 1607
QY 1548 GACGGGCTGAGCCACTGGTCACTTGGTCTTCACTGCTGTGACCTGTGGATTGGC 1607
Db 1803 GACGGGCTGAGCCACTGGTTCGCGCTGCTCTGCTGCTAGTACCTGCGCGCTCGCG 1862
QY 1608 AATATCACACGATCCGCTCTGCAACTCCCAAGTCCCAAGTCCCAAGTCCCAAGTCCCA 1667
Db 1863 AACGTCACCCGCTATCCGCTCTGCAACTCCCAAGTCCCAAGTCCCAAGTCCCAAGTCCCA 1922
QY 1668 AAGGGAGTGGCCGGGAGACCAAGCCCTGCCAGSGCGCCCAATGCTGATGGCCGC 1727
Db 1923 AAGGGAGTGGCCGGGAGACCAAGCCCTGCCAGSGCGCCCAATGCTGATGGCCGC 1982
QY 1728 TGGACCCCTGCTCCCGTGGTGGCCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1787
Db 1983 TGGACCCCTGCTCCCGTGGTGGCCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2042
QY 1788 CCGACCCCGGCTGTCACAGCCCTGAGCTCAGTACGAGGAGGAGGCTGCTGCTGCTGCTGCTG 1847
Db 2043 CGGACAGCGCTTGCACAGCCCGGAGCCCGAGCCAGCGGGGAGGAGTGCCTGCGGGGGC 2102
QY 1848 GTGAGGAGCGCTCAGATGTCAACAGAGGAGCTGCCCGCTGGATGGCTGTTTATCCAAAC 1907
Db 2103 GCCAAGGAGCAACAGATGTCAACAGGAGAGCTGCCCGCATAGAGCGCTGCTGTCACAC 2162
QY 1908 CCTGCTTCCCGGAGCCAGTGCAGAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCTGCTG 1967
Db 2163 CCTGCTTCCCGGAGCTGAGTGCAGAGCTTCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2222
QY 1968 TGCCCTGTGGGCTTCTTGGGAAATGGCAACCTGCTGAGGAGCTGAGAGAGTGTGCCCTG 2027
Db 2223 TGCCCGGGGGCTTCTTGGGAAATGGCAACCTGCTGAGGAGCTGAGAGAGTGTGCCCTG 2282
QY 2028 GTCCCGGAGCTGCTTCTCCACAGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2087
Db 2283 GTGAGGAGCTGCTTCTCCACAGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2342
QY 2088 TTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2147
Db 2343 TACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2402
QY 2148 GAAGCAGCAAGAGGAAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGAGCAAGACA 2207
Db 2403 GAGGGGCGAGGACTGAGAACAGGTGTGTGAGCCCGGAGAACCCCTGCAAGGAGCAAGACC 2462
QY 2208 CACAACTGCCACAGCAGCGGAGTGCATCTACCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2267
Db 2463 CACAGCTGCCACCGGAGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2522
QY 2268 AAGTCCGAGTCCGACAGAGGCTAGCGGGCGAGCGGCTCATCTGCGGGGAGGACTCGGAC 2327
Db 2523 AAGTCCGAGTCCGACAGAGGCTAGCGGGGTGACGGGCTCATCTGCGGGGAGGACTCGAGAC 2582
QY 2328 CTGGACGGCTGGCCCAACCTCAATCTGGTGTGCGCCACCAACGCGACCTACCACTGCATC 2387
Db 2583 CTGGATGGCTGGCCCAACCAAGACCTGTGTGCGCCACCAACGCGACCTACCACTGCATC 2642
QY 2388 AAGGATACTGCCCGGCTGCTGCCAAATCTTGGGAGGAGAGTGTGCAAGGAGCGGAT 2447
Db 2643 AAGGATACTGCCCGGCTGCTGCCAAATCTTGGGAGGAGAGTGTGCAAGGAGCGGAT 2702
QY 2448 GCGCATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2507

Db 2703 GGGGACGGCTGCGAGAGGAGATGACAAACGAGCGGCTCTCGAGAGAGAGCAACTGC 2762
QY 2508 CAGCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAAGATGAGTTGGGAGCGCTGT 2567
Db 2763 CAGCTTCTCTTCAACCCCGCTCAGTTCGACTACGACAAAGATGAGTTGGGAGCGGCTGC 2822
QY 2568 GACAACTGCCCTTACGTGCACAAACCTGCCAGATGCCACAGACAAACAAATGAGAGGT 2627
Db 2823 GACAACTGCCCTTATGTTTCAAAACCGGCGGAGATGCACAGGACAAACAAACGCGGAGGT 2882
QY 2628 GACGGCTGCTCGGTGGACATGATGGGAGCGATGCTTCAATGAAAGAGACAAATGTCGCC 2687
Db 2883 GACGGCTGCTCGGTGGACATGACGGGAGCGATGCTTCAACGAGCGAGACAACTGTCGCC 2942
QY 2688 TACGCTTCAACACATGACAGAGGAGACGAGTGTGAGCGGTGTGGGGATCAGTGTGAC 2747
Db 2943 TACGCTTCAACACCGGAGCGGAGCGGAGCGGCTGGGTGACCACTGTGAC 3002
QY 2748 AACTGCCCTGCTGTCACAAACCTGACAGACCGAGCGTGGACAAATGACCTTGTGGGAG 2807
Db 3003 RACTGTGCTGCTGTCACAAACCGGAGCGGAGCGGAGCGTGGAGCAACGCTGTGGGAGAC 3062
QY 2808 CAGTGTGACAAACAGAGGAGATAGATGACGAGCGGCGCCAGACAAACAGGAGCAACTGC 2867
Db 3063 CAGTGTGACAAACAGAGGAGATGACGAGCGGCGCCAGGAGCAACAGGAGCAACTGC 3122
QY 2868 CCTACATCTCCAACGCCCAACGAGCTGACCATGACAGAGCGGCGGAGCGGAGCGGCTGT 2927
Db 3123 CCCCACATCCCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGCTGT 3182
QY 2928 GACCTGATGATGACAAACGAGTGGCTGCCCGATGACAGGAGCAACTGCGGCTGTGTTC 2987
Db 3183 GACTGGGAGCGGAGCAATGATGGGATCCCGAGCAGGAGCAACTGCGGCTGTGTTCGCC 3242
QY 2988 AACCAGACAGGAGGAGTGGACGGTATGAGCGGGGTGATATTTGTAAGATGATTTT 3047
Db 3243 AACCCGAGCGGAGGAGTGGACGGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCTTC 3302
QY 3048 GACAAATGACAACTCCCGAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3107
Db 3303 GACAAAGAGAGTATTCCTGATATGACAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3362
QY 3108 ACAGACTTCAGAACTTCCAGATGCTGCCCTTGGATCCCAAGGAGCAACCCAAATGAT 3167
Db 3363 ACAGACTTCAGAACTTCCAGATGCTGCCCTTGGATCCCAAGGAGCAACCCAAATGAT 3422
QY 3168 CCCAACTGGGTTCATTCGCCATCAAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3227
Db 3423 CCCAACTGGGTTCATTCGCCATCAAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3482
QY 3228 GGCATCGCTGTAGTGTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3287
Db 3483 GGCATCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3542
QY 3288 AACACTGACCGGAGCGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3347
Db 3543 AACAGGAGCGGAGCGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3602
QY 3348 TTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3407
Db 3603 TTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3662
QY 3408 GCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3467
Db 3663 GCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3722
QY 3468 CACTGAGGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3527
Db 3723 CACTGAGGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3782
QY 3528 CACGACCGGAGCAATTTGGTGGAGGAGTACACGCGCTATAGGTGGCAGCTGACTCAC 3587

| | | | |
|---|--|--|-------------|
| Db | 3783 | CACGACCCCAAGAAATATCGGCTGGAAGGACTACACTGCGCTACCGGTGGCATCTGACCCAC | 3842 |
| Qy | 3588 | AGGCCCAAGACCGGCTACATCAGAGTCTTAGTGATGAGGAAACAGGTCATGGCAGAC | 3647 |
| Db | 3843 | AGGCTTAAGACAGGCTACATAAGAGTCTTAGTACATGAAGGAAACAAAGTCATGGCGAC | 3902 |
| Qy | 3648 | TCAGGACCTATCTATGACCAAACTACGCTGGCGGGGGCTGGGTCTATTGTTCTTCTCT | 3707 |
| Db | 3903 | TCAGGACCCATCTATGACCAAACTACGCTGGTGGGGCGCTGGGTCTGTTTGTCTCTCT | 3962 |
| Qy | 3708 | CAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCAGAGATATTTAAACAAGATTT | 3767 |
| Db | 3963 | CAAGAGATGGTCTACTTCTCGGACCTCAAAATATGAATGACAGAGATGCTTAAGCAAGATTT | 4022 |
| Qy | 3768 | GCTGCATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACACCTCAGTTCATTTGTG | 3827 |
| Db | 4023 | GCTGTGTTTCCAGCAAGTAGTGTAAATGC--TGTATCCCAACACCTCAGTCCATCCCA | 4080 |
| Qy | 3828 | GTCTTGGGGTCTCTCTCTTAGCAGCACCTCTCTGCTCCCTTGACCTTAACCTCTGATGTT | 3887 |
| Db | 4081 | GTGCTTCAGCTATCTCTCTAGCA--AACCTCTATCCCTGACCCCTAACCTGAGTGGTT | 4138 |
| Qy | 3888 | CTTCACCTCTCCGACGAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGA | 3947 |
| Db | 4139 | CTTCACCTGCTGCTCTCAA--CCCAAGCCCAATTGCTTCAGAGGATAAATAATGGA | 4197 |
| Qy | 3948 | CTCAGAGATGAACATCTAACCCACTAGAGG-AAACCCAGTTTGGTGATATATGAGACTTTA | 4006 |
| Db | 4198 | CTGAAGATGAACGCTCCAAACCCACTACAGGAAAGCAGTTTGAGAACCCACGAGACTTCA | 4257 |
| Qy | 4007 | TGTGGAGTGAATTTGGGATGCCATGACATTGCT---TTTTCTGTTGTTTAAAAAG | 4062 |
| Db | 4258 | TGTGGAGTGAATTTGACATGATGATGTTTCTTTCTTTCTGTTTAAAAAG | 4317 |
| Qy | 4063 | AATGACGTTTACATATAAATG | 4084 |
| Db | 4318 | AATGACGTTTACATATAAATG | 4339 |
| RESULT 7 | | | |
| HUMTHRSPD | | | |
| LOCUS | HUMTHRSPD 2780 bp mRNA linear PRI 03-AUG-1993 | | |
| DEFINITION | Human thrombospondin mRNA. | | |
| ACCESSION | M81339 | | |
| VERSION | M81339.1 GI:339678 | | |
| KEYWORDS | thrombospondin. | | |
| SOURCE | Homo sapiens adult connective cDNA to mRNA. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| AUTHORS | LaBell,T.L., Milewicz,D.J., Distche,C.M. and Byers,P.H. | | |
| TITLE | Thrombospondin II: partial cDNA sequence, chromosome location, and expression of a second member of the thrombospondin gene family in humans | | |
| JOURNAL | Genomics 12 (3), 421-429 (1992) | | |
| MEDLINE | 92217961 | | |
| PUBMED | 1559694 | | |
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| BASE COUNT | 732 a | 723 c | 724 g 601 t |
| ORIGIN | | | |
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| Best Local Similarity 100.0%; Pred. No. 0; | | | |
| Matches 2778; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| Qy | 1916 | CCCGGGAGCCAGTGCAGCAGCTTCCCGGATGGGTCTGGTCAATGGCGCTTCTGCCCTGT | 1975 |

| | | | |
|----|------|---|------|
| Db | 1 | CCCCGGAGCCAGTGCAGCAGCTTCCCCGATGGGTCTTGGTCAATGGCGCTTCTGCCCTGT | 60 |
| Qy | 1976 | GGGCTTCTTGGGCAATGSCACCCACTGTGAGGACCTTGAGCAGTGTGCCCTGGTCCCGA | 2035 |
| Db | 61 | GGGCTTCTTGGGCAATGSCACCCACTGTGAGGACCTGTGACGAGTGTGCCCTGGTCCCGA | 120 |
| Qy | 2036 | CATCTGCTTCTCCACCAGCAAGGTGCTTGGTGTCAACTCAGCCTCAGCCTGGCTTCCACTG | 2095 |
| Db | 121 | CATCTGCTTCTCCACCAGCAAGGTGCTTGGTGTCAACTCAGCCTCAGCCTGGCTTCCACTG | 180 |
| Qy | 2096 | CTGCGCTTCCCGCCCGCCATACAGAGGGAACAGCCCTCGGGGTGCGCTTGAAGAGCAGC | 2155 |
| Db | 181 | CTGCGCTTCCCGCCCGCCATACAGAGGGAACAGCCCTCGGGGTGCGCTTGAAGAGCAGC | 240 |
| Qy | 2156 | CAAGCAGGAAAGCAAGTGTGTGAGCCGCGGAAACCCATGCAAGGACAAAGACACAACTG | 2215 |
| Db | 241 | CAAGCAGGAAAGCAAGTGTGTGAGCCGCGGAAACCCATGCAAGGACAAAGACACAACTG | 300 |
| Qy | 2216 | CCAAAGCAGCGGAGTGCATCTACCTGGGTCACTTACAGGACCCCATGTACAAGTGGGA | 2275 |
| Db | 301 | CCAAAGCAGCGGAGTGCATCTACCTGGGTCACTTACAGGACCCCATGTACAAGTGGGA | 360 |
| Qy | 2276 | GTGCCAGACAGCTACGCGGCGGAGGCTCATCTCGCGGAGGAGTCTGACCTCGGAGG | 2335 |
| Db | 361 | GTGCCAGACAGCTACGCGGCGGAGGCTCATCTCGCGGAGGAGTCTGACCTCGGAGG | 420 |
| Qy | 2336 | CTGCGCCCAACTCAATCTGCTGCGCCCAACCAACCCACTTACCACTGCATCAAGGATAA | 2395 |
| Db | 421 | CTGCGCCCAACTCAATCTGCTGCGCCCAACCAACCCACTTACCACTGCATCAAGGATAA | 480 |
| Qy | 2396 | CTGCGCCCATCTGCCAAATCTTGGCAGAGAGACTTTTACAAGAGCGGATGGCGATGC | 2455 |
| Db | 481 | CTGCGCCCATCTGCCAAATCTTGGCAGAGAGACTTTTACAAGAGCGGATGGCGATGC | 540 |
| Qy | 2456 | CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 2515 |
| Db | 541 | CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 600 |
| Qy | 2516 | CTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTGTGGGACCGCTGTGCAAACTG | 2575 |
| Db | 601 | CTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGGTGTGGGACCGCTGTGCAAACTG | 660 |
| Qy | 2576 | CCCTTACGTGCACAACTCTGCCAGATGCACACAGACAAATGAGAGGGTGCAGCCTG | 2635 |
| Db | 661 | CCCTTACGTGCACAACTCTGCCAGATGCACACAGACAAATGAGAGGGTGCAGCCTG | 720 |
| Qy | 2636 | CTCGTGGACATTTGATGGGAGGATGCTTCAATGAACAGAGCAATTTCCCTACGCTTA | 2695 |
| Db | 721 | CTCGTGGACATTTGATGGGAGGATGCTTCAATGAACAGAGCAATTTCCCTACGCTTA | 780 |
| Qy | 2696 | CAACACTGACAGAGGACAGGATGAGGTGTGGGATGATGATGATGATGATGATGATGATG | 2755 |
| Db | 781 | CAACACTGACAGAGGACAGGATGAGGTGTGGGATGATGATGATGATGATGATGATGATG | 840 |
| Qy | 2756 | CCTGTGACAACTCTGACAGACCGAGCTGACAAATGACCTTGTGGGACCACTGTGA | 2815 |
| Db | 841 | CCTGTGACAACTCTGACAGACCGAGCTGACAAATGACCTTGTGGGACCACTGTGA | 900 |
| Qy | 2816 | CAACACGAGGACATAGATGACAGGCGCACAGAACACAGGACAACTGCCCTTACAT | 2875 |
| Db | 901 | CAACACGAGGACATAGATGACAGGCGCACAGAACACAGGACAACTGCCCTTACAT | 960 |
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| Db | 961 | CTCCAACGCCCAACAGGCTGACCATGACAGAGACGGCGGACGCGCTGTGACCCCTGA | 1020 |
| Qy | 2936 | TGATGACAACTGCGCTTCCCGATGACAGGACAACTTCCCGGCTGTGTTCAACCCAGA | 2995 |
| Db | 1021 | TGATGACAACTGCGCTTCCCGATGACAGGACAACTTCCCGGCTGTGTTCAACCCAGA | 1080 |
| Qy | 2996 | CCAGGAGACCTTGGACGCTGATGGAGCGGCTGATATTTGTTAAAGATGATTTTGAATGA | 3055 |

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| Db | 1081 | CCAGGAGGACTTGGACGGTGTAGCGGCGGTGATATTTGCTAAAGATGATTTTGACAAATGA | 1144 |
| Qy | 3056 | CAACATCCCAGATATTGATGATGTGTGCTCTGAAACCAATGCCATCAGTGAGACAGACTT | 3115 |
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| Qy | 3116 | CAGGAATCCAGATGGTCCCTTGGATGCCAAAGGGACCAACC0AAATTGATCCCAACTG | 3175 |
| Db | 1201 | CAGGAATCCAGATGGTCCCTTGGATGCCAAAGGGACCAACC0AAATTGATCCCAACTG | 1260 |
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| Db | 1261 | GGTCATTCCGCAATCAGGCAAGGAGCTGGTTCAGACACGCCAACTCGGACCCCGGCATCGC | 1320 |
| Qy | 3236 | TGTAGGTTTTGACGAGTTTTGGGTCTGTGGACTTTCAGTGGCACATCTTACGTAACACTGA | 3295 |
| Db | 1321 | TGTAGGTTTTGACGAGTTTTGGGTCTGTGGACTTTCAGTGGCACATCTTACGTAACACTGA | 1380 |
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| Db | 1381 | CCGGGACGAGCAATGCTGGGCTTCGTCTTTGGTTTAC0AGTCAAGACGCGCTTCTATGT | 1440 |
| Qy | 3356 | GGTGATGTGGAAGCAGGTGACGACAGCTACTGGGAGGACAGCCCGGCGGCTATGG | 3415 |
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| Qy | 3416 | CTACTCCGGCGTCTCCCTCAAGGTGGTGAACCTCCACCACGGGGACGGGCGAGACCTGAG | 3475 |
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| Qy | 3836 | GGCTTCTCTCTTAGCAGACCTCCTGTGCCCTTGACCTTAACTCTGATGTTCTTCAACCT | 3895 |
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| Qy | 4256 | TATAACAAGGGTCCAATTCAAATTTGAAGTAAATGTTTTAGTAAGGAGAGATTAGAAGACA | 4315 |
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| Qy | 4436 | AGTTTTCATAAAGAACAAACATCCTTGCMAATGGGTGTGACGCGGTTCCAGATGTGGATT | 4495 |
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| Qy | 4556 | TTGTGCGGTGTGTGGGTCGGGAGGCTTCCTGCCGTAGCTTCCTTCCCAGCTTTCCTGCC | 4615 |
| Db | 2641 | TTGTGCGGTGTGTGGGTCGGGAGGCTTCCTGCCGTAGCTTCCTTCCCAGCTTTCCTGCC | 2700 |
| Qy | 4616 | TGAGAGGAACAGAGCAGACGACAGCGCGGAAAGGCGCATCTTAAGCGCTATCTAGGCT | 4675 |
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RESULT 8
MUSTSP2B
LOCUS
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VERSION
KEYWORDS
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ORGANISM
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AUTHORS
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JOURNAL
MEDLINE
PUBMED
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FEATURES
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 Laherty,C.D., O'Rourke,K., Wolf,F.W., Katz,R., Seldin,M.F. and
 Dixit,V.M.
 1 (bases 1 to 4108)
 Characterization of mouse thrombospondin 2 sequence and expression
 during cell growth and development
 J. Biol. Chem. 267 (5), 3274-3281 (1992)
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| Qy | 1966 | TCGCCCCGTGGGCTTCTTGGGCAATGGCACCACTGTGAGGACTGTGACGAGTGTGCC | 2025 |
| Db | 1945 | CTTGCCCACTGGGCTTCTTGGGCAATGGTACCCACTGTGAGGACTGGATGAGTGTGCTG | 2004 |
| Qy | 2026 | TGTTCCCCGACATGCTGTTCTCCACAGCAAGGTGCCCTCGCTGTGTCAACACTCAGCCTG | 2085 |
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| SOURCE | chicken, cdna to mRNA. |
| ORGANISM | Gallus gallus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; |
| AUTHORS | Phasianinae; Gallus. |
| TITLE | 1 (bases 1 to 3537) |
| JOURNAL | Lawler, J., Duquette, M. and Ferro, P. Cloning and sequencing of chicken thrombospondin J. Biol. Chem. 266 (13), 8039-8043 (1991) MEDLINE 91217026 |
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RESULT 10
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ACCESSION G06722
VERSION G06722.1 GI:859967
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hudson.T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GCAGGAATAGTCACTCATCC
Primer B: TTGACCCACACACAGAAA
STS size: 347
PCR Profile:
 Presoak:
 Denaturation:
 Annealing: 56 degrees C
 Polymerization:
 PCR Cycles: 35
 Thermal Cycler:
Protocol:
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 dNTPs: each 4 nM
 Taq Polymerase: 0.025 units/ul
 Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from L12350 -- Unigene.
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| Db | 1861 | CAAAATTTATCGTATAGGTTGATGAACGTCATGCTTTTGGCAAGACTGTAAATATTTA | 1920 |
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| ACCESSION | M64866 | | |
| VERSION | M64866.1 GI:201994 | | |
| KEYWORDS | thrombospondin. | | |
| SOURCE | Mus musculus cDNA to mRNA. | | |
| ORGANISM | Mus musculus | | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| REFERENCE | 1 (bases 1 to 2837) | | |

| | | | |
|-----------------------|---|---|---------------------|
| AUTHORS | Bornstein, P., O'Rourke, K., Wikstrom, K., Wolf, F.W., Katz, R., Li, P. and Dixit, V.M. | | |
| TITLE | A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome | | |
| JOURNAL | J. Biol. Chem. 266 (20), 12821-12824 (1991) | | |
| MEDLINE | 91302287 | | |
| PUBMED | 1712771 | | |
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RESULT 12

AB005287

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus mRNA for thrombospondin 1, complete cds.

AB005287

AB005287.2

GI:4630795

Bos taurus (strain:Holstein) two weeks after birth male anterior

tooth odontoblast cDNA to mRNA, clone:pTSL-28.

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (sites)

Ueno,A., Yamashita,K., Nagata,T., Tsurumi,C., Miwa,Y., Kitamura,S.

and Inoue,H.

cDNA cloning of bovine thrombospondin 1 and its expression in

odontoblasts and prederitin

Biochim. Biophys. Acta 1382 (1), 17-22 (1998)

98173773

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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source

CDS

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Matches 2392; Conservative 0; Mismatches 1193; Indels 32; Gaps 4;

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DEFINITION Sequence 1 from Patent WO0118250.
ACCESSION AX094823
VERSION AX094823.1 GI:13511028
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5722)
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and
McCarthy, J.J.

TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
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DEFINITION Sequence 3704 from Patent WO0229103.
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VERSION AX411057.1 GI:21443762
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3704 11-APR-2002;
JOURNAL GENE LOGIC INC (US)
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BASE COUNT 1514 a 1388 c 1387 g 1433 t
ORIGIN

Query Match 26.8%; Score 1550.4; DB 6; Length 5722;
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Matches 2326; Conservative 0; Mismatches 1171; Indels 33; Gaps 4;

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| Db | 1552 | ACCAAGCCTTGCAAGAAAGACGCTTGCCCCATCAATGAGGCTGGGTCTTGTGTCAACA | 1611 |
| Qy | 1746 | TGTTGGCCTTGCACTGTCACTGTGCGGTGGGATCCGGGAGCGCACCCGGGTCTGCAAC | 1805 |
| Db | 1612 | TGGGACATCTGTCTGCTCACTGTGAGGAGGGTACAGAAACGTAGTCTCTGCAAC | 1671 |
| Qy | 1806 | AGCCTGAGCCTCAGTACGAGGAGGAGCGCTCGGTGGGGATGTGAGGAGCGTFCAGATG | 1865 |
| Db | 1672 | AAOCCGACACCCAGTTTGGAGCAAGGACTCGTGTGTGTATGATGTAACAGAAAACCAATC | 1731 |
| Qy | 1866 | TGCAACAAGAGGAGTGCCTCGCTGGATGCTTTATCCAAACCTCTGCTTCCCGGGAGCC | 1925 |
| Db | 1732 | TGCACAAAGCAGACTGTCCAATGATGATGCTGTCCAATCCCTGCTTTCGCGGGGTG | 1791 |
| Qy | 1926 | CAGTGCAGCAGCTTCCCGATGGTCTGTGTCATCGGCTTCTGCCCTGTGGGCTTCTTG | 1985 |
| Db | 1792 | AAGTGTACTAGCTACCTGATGSCAGCTGGAATATGTGTCTGTGCCCTGGTTTACAGT | 1851 |
| Qy | 1986 | GGCAATGGCACCCACTGTGAGAGACCTGNCAGAGTGTGCCCTGTGCCGAGATCTGCTTC | 2045 |
| Db | 1852 | GGAAATGGCATCCAGTGCACAGATGTGATGAGTGCAAAGAGTGCCTGTATGCTGTCTC | 1911 |
| Qy | 2046 | TCACACAGCAAGGTGCTCGCTGTGTCAACACTCAGCCTGGCTTCCACTGCTGSCCTGC | 2105 |
| Db | 1912 | AACCACATGGAGAGCACCGTGTGAGAACACGGACCCCGGCTACACTGCTTCCCTGTC | 1971 |
| Qy | 2106 | CCGCCCGGATACAGAGGGAACCAACCGTTCGGGGTTCGCCCTGGAAGCAGCAAGACGGAA | 2165 |
| Db | 1972 | CCCCACGCTTACACGGCTCACAGCCTTCGSCCAAGGTTGCAACATGCCACGGCCAAC | 2031 |
| Qy | 2166 | AAGCAAGTGTGAGCCCCGAAACCCATGCAAGGACACAGACACACTGCCACAGCAC | 2225 |
| Db | 2032 | AAACAGTGTGCAAGCCCCGTAAACCCCTGCACGGATGGGACCCACGACTGCAACAAGAC | 2091 |
| Qy | 2226 | CGGAGTGTACTTACCTGGTCACTTCAGCAGACCCATGTACAAGTGGAGTGCACACA | 2285 |
| Db | 2092 | GCCAGTGCACACTTCTTGGCCACTATACGACCCCATGTACCGCTGGAGTGCAGCCT | 2151 |
| Qy | 2286 | GGCTACGCGGGACCGGCTCATCTCGGGGAGGACTCGGACCTGGAGCGGTGCCCCAAC | 2345 |
| Db | 2152 | GGCTACGCTGGCAATGGCATCATCTCGGGGAGGACACAGACCTGGATGGCTGGCCCCAAT | 2211 |
| Qy | 2346 | CTCAACTTGTCTGCCCAACCAAGCCACCTTACACTGCATCAGGATTAACCTGCCCCCAT | 2405 |
| Db | 2212 | GAGAACTGGTGTGCTGGCCAAATCGACTTACCACTGCAAAAGGATTAATTTGCCCAAC | 2271 |

| | | | |
|----|------|---|------|
| QY | 2406 | CTGCCAAATTTCTGGCGAGGAAAGACTTTTGACAAGAGACGGGATTTGGCGATGCCCTGTGATGAT | 2466 |
| DB | 2272 | CTTCCCAACTCAGGGCAGGAAGAACTATGACAAGGATGGAAATTTGGTGTGATTTGGCTGTGATGAT | 2331 |
| QY | 2466 | GACGATGACAATGACGGTGTGACCGATGAGAAGGACAACCTGCCAGCTCCTCTTCAATCCC | 2525 |
| DB | 2332 | GACGATGACAATGATAAAATTCAGATGACAGGGACAACCTGTCCATTCATTTACAACCCA | 2391 |
| QY | 2526 | CGCCAGGCTGACTATGACAAGGATGAGTTTGGGGACCGCTGTGACAACCTGCCCTTACGTG | 2585 |
| DB | 2392 | GCTCAGTATGACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACCTGTCCCTACAA | 2451 |
| QY | 2586 | CACAACCCCTGCCAGATCGACACAGACAACAATGAGAGGGTGAGCCCTGCTCCGTGGAC | 2645 |
| DB | 2452 | CACAAACCCAGATCAGGCGACAGACAACAATGGGAGAGAGAGCCCTGTGCTGCAGAC | 2511 |
| QY | 2646 | ATTGATGGGACGATGCTTCAATGAACGAGACAATTTGCCCTACGCTGTACAACACATGAC | 2705 |
| DB | 2512 | ATTGATGGAGACGGTATCTTCAATGAACGGGACAACCTGCCAGTAGCTGTACAATGTGGAC | 2571 |
| QY | 2706 | CAGAGGACACGGATGGTGTGACGGTGTGGGGGATCACTGTGACAACCTGCCCTTGGTGAC | 2765 |
| DB | 2572 | CAGAGAGACACTGATATGGATGGGTTTGGAGATCAGTGTGACAATTTGCCCTTGGACAC | 2631 |
| QY | 2766 | AACCCCTGACGAGACCGACGTGGGACAATGACCTTTGTTGGGACAGAGTGACACAACGAG | 2825 |
| DB | 2632 | AATCCGATCAGCTGGACTGTGACTCAGACCGCAATTTGGAGATACCTGTGTGACAACATCAG | 2691 |
| QY | 2826 | GACATAGTGNACGACGCCACAGACAACACAGGACAACCTGCCCTACATCTCCAACGCC | 2885 |
| DB | 2692 | GATATTGATGAAGATGGCCACCAAGACAATCTGGACAACCTGTCCCTATTTGCCCAATGCC | 2751 |
| QY | 2886 | AACCAAGCTGACCATGACAGACGCGCCAGGGCGACGCTGTGACCCCTGATGATGACAAC | 2945 |
| DB | 2752 | AACCAAGCTGNCCATGACAAGATGGCAAGGAGATGCTGTGACCAGATGATGACAAC | 2811 |
| QY | 2946 | GATGGCTGCCGATGACAGGGACAACCTGCCGGCTGTGTTCACCCAGACAGGAGGAC | 3005 |
| DB | 2812 | GATGGCATTCCTGATGACAAGGACAACCTGCACACTCGTGCCCAATCCCGACAGAAAGAC | 2871 |
| QY | 3006 | TTGACAGGTGATGGACGGGTGATATTTGTAAGATGATTTTGACAATTGACAACATCCCA | 3065 |
| DB | 2872 | TCTGACGGCATGGTCAGGTGATGGCTGCAAGATGATTTTGACCATTGACAGTGTGCCA | 2931 |
| QY | 3066 | GATATTGATGATGTGTCTGTAACAAATGGCCATGAGTGAAGACAGCTTCAGGAACCTC | 3125 |
| DB | 2932 | GACATCATGATCATCTGTCTGAGATGTTGATCATGAGAGACCGATTTCCGCGGATTC | 2991 |
| QY | 3126 | CAGATGTCCTTTGGATCCCAAGGGACCCCAAAATTTGATCCCACTGGGTCTATTCGC | 3185 |
| DB | 2992 | CAGATGATTCCTCTGGACCCCAAGGGACATCCCAAAATGACCCCTAACTGGGTTGTACGC | 3051 |
| QY | 3186 | CATCAAGCCAGGACGTGTTTACAGACAGCCAACCTCGGACCCCGGCATCGCTGTAGGTTT | 3245 |
| DB | 3052 | CATCAGGGTAAAGAACTCTGCCAGACTGTCAACTGTGATCTCTGGACTCGCTGTAGGTTAT | 3111 |
| QY | 3246 | GACGAGTTTGGGTCTGTGGACTTCAGTGGCAATTTCTAGTAAACACTGACCCGGAGCAC | 3305 |
| DB | 3112 | GATGAGTTTAACTGTGTGGACTTCAGTGGCACTTCTTTCATCATCACCCGAAGGACGAT | 3171 |
| QY | 3306 | GACTATGCTGGCTTCGTCTTTTGGTTTACCAGTCAAGCAGCCGCTTCTATGTGGTGTGG | 3365 |
| DB | 3172 | GACTATGCTGGATTTGTCTTTTGGCTTACCAGTCCACGACCGCGCTTTTATGTTGTATGG | 3231 |
| QY | 3366 | AAGCAGGTGACGAGACCTTACTGGGAGGACCAAGCCACCGCGGCCCTATGGCTACTTCGGC | 3425 |
| DB | 3232 | AAGCAAGTCAACCAGTCTCTACTGGGACACCAACCCACGAGGGCTACAGGGATACTCGGC | 3291 |
| QY | 3426 | GTGTCCCTCAAGTGTGTAACTCCACCGGGAGCGGGAGCACCTGTGAGAAGCGCTG | 3485 |
| DB | 3292 | CTTTCTGTGAAGTGTGAAACTCCACCAAGGGCTTGGCGAGACCTGTGGGAAGCGCCT | 3351 |
| QY | 3486 | TGGCACACGGGGAACACCGCCGGGCGAGGTGGCAACTTTATGGCACACGCCCCAGGAACATT | 3545 |

| | | | |
|----|------|---|------|
| Db | 3352 | TGGCACAAGAAACACCCCTGGCAGGTGGCCACCTGTGGCATGACCTCGTGCACATA | 3411 |
| Qy | 3546 | GGCTGGAAGGACTACACGGCCCTATAGGTGGCACCTGACTCACAGGCCCAAGACCGGCTAC | 3605 |
| Db | 3412 | GGCTGGAAGAATTTCACCCCTTCACAGATGGGTCTCAGCCACAGGCCAAAGACGGGTTC | 3471 |
| Qy | 3606 | ATCAGAGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACTCAGGACCTATCTATGAC | 3665 |
| Db | 3472 | ATTAGAGTGGTGATGTATGAAGGGAAGAAATCATGGCTGACTCAGGACCCATCTATGAT | 3531 |
| Qy | 3666 | CRAACCTAGCTGGGGGGGGCTGGGTCTATTGTCTCTCTCAAGAAATGGTCTATTTC | 3725 |
| Db | 3532 | AAACCTATGCTGGTGGTAGACTAGGGTGTGTGTCTCTCAAGAAATGGGTGTTCTTC | 3591 |
| Qy | 3726 | TCAGACCTCAAGTACGAATGACAGAGATATTTAAACAAGATTGCTGCATT | 3775 |
| Db | 3592 | TCTGACCTGAAATAGCAATGTAGAGATCCCTAATCATCAAAATCTTGATT | 3641 |

Search completed: December 27, 2002, 03:13:33
Job time : 9631 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:12:49 ; Search time 725 Seconds

(Without alignments)

17966.287 Million cell updates/sec

Title: US-09-919-770-3

Perfect score: 5784

Sequence: 1 acggcatccagtcacagagg.....aattgtaaaaagggtttct 5784

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 5784 | 100.0 | 5784 | 24 | Gene #2160 used to |
| 2 | 5784 | 100.0 | 5784 | 24 | Human cDNA encodin |
| 3 | 5784 | 100.0 | 5784 | 24 | Colon adenocarcino |
| 4 | 3683.4 | 63.7 | 3787 | 21 | Human cancer assoc |
| 5 | 3573.6 | 61.8 | 3596 | 21 | Human thrombospond |
| 6 | 3404.8 | 58.9 | 3522 | 22 | Human colon cancer |
| 7 | 2745.2 | 47.5 | 4108 | 22 | Human METH1 relate |
| 8 | 2745.2 | 47.5 | 4108 | 22 | L07803 CDNA clone. |
| 9 | 2731.8 | 47.2 | 4170 | 24 | Rat cDNA isolated |

| | | | | | | |
|----|--------|------|------|----|-----------|--------------------|
| 10 | 1872 | 32.4 | 2837 | 20 | AAZ32015 | Human METH1 relate |
| 11 | 1872 | 32.4 | 2837 | 22 | AAZ90072 | M64866 CDNA clone. |
| 12 | 1604.2 | 27.7 | 5289 | 20 | AAZ32052 | Human METH2 relate |
| 13 | 1604.2 | 27.7 | 5289 | 22 | AAZ90309 | AB005287 CDNA clon |
| 14 | 1550.4 | 26.8 | 5721 | 22 | AAH02923 | Human shear stress |
| 15 | 1550.4 | 26.8 | 5722 | 22 | AAZ32012 | Human METH1 relate |
| 16 | 1550.4 | 26.8 | 5722 | 22 | AAZ95238 | Human variant thro |
| 17 | 1550.4 | 26.8 | 5722 | 22 | AAZ90069 | X14787 CDNA clone. |
| 18 | 1550.4 | 26.8 | 5722 | 22 | AAZ90069 | Gene #3704 used to |
| 19 | 1548.8 | 26.8 | 4433 | 20 | AAZ32014 | Human METH1 relate |
| 20 | 1548.8 | 26.8 | 4433 | 22 | AAZ90071 | X04665 CDNA clone. |
| 21 | 1548.8 | 26.8 | 6132 | 23 | ABV24661 | Human prostate exp |
| 22 | 1548.8 | 26.8 | 7232 | 24 | AAZ94912 | Human DNA sequence |
| 23 | 1529.8 | 26.4 | 5830 | 21 | AAZ77811 | Human cancer assoc |
| 24 | 1522.2 | 26.3 | 4339 | 20 | AAZ32054 | Human METH2 relate |
| 25 | 1522.2 | 26.3 | 4339 | 22 | AAZ90311 | M87276 CDNA clone. |
| 26 | 684.6 | 11.8 | 2468 | 22 | AAZ90613 | Angiotensin conver |
| 27 | 651.8 | 11.3 | 713 | 22 | AAZ34534 | Human colon cancer |
| 28 | 601.6 | 10.4 | 2439 | 24 | ABL62104 | Colon adenocarcino |
| 29 | 601.6 | 10.4 | 2439 | 24 | ABL62870 | Breast cancer rela |
| 30 | 601.6 | 10.4 | 2439 | 24 | ABL63089 | Breast cancer rela |
| 31 | 595.6 | 10.3 | 619 | 21 | AAA78040 | CDNA encoding huma |
| 32 | 595.6 | 10.3 | 619 | 22 | AAI28778 | Colon tumour relat |
| 33 | 594.8 | 10.3 | 848 | 20 | AAZ17196 | Human gene express |
| 34 | 566.6 | 9.8 | 2563 | 22 | AAZ94255 | Human full-length |
| 35 | 559.4 | 9.7 | 3074 | 15 | AAZ94255 | Human thrombospond |
| 36 | 559.4 | 9.7 | 3074 | 24 | ABL69126 | Kidney cancer rela |
| 37 | 559.4 | 9.7 | 3434 | 22 | AAZ95239 | Human variant thro |
| 38 | 545.6 | 9.4 | 2916 | 22 | AAZ52211 | Human polynucleoti |
| 39 | 540.2 | 9.3 | 637 | 23 | AAZ58772 | CDNA #1448 encodin |
| 40 | 526.4 | 9.1 | 2820 | 15 | AAZ966454 | Xenopus thrombospo |
| 41 | 526 | 9.1 | 2053 | 20 | AAZ32053 | Human METH2 relate |
| 42 | 526 | 9.1 | 2053 | 22 | AAZ90310 | X87619 CDNA clone. |
| 43 | 516 | 8.9 | 516 | 24 | ABK45682 | CDNA encoding colo |
| 44 | 514.6 | 8.9 | 925 | 21 | AAA47735 | Human COMP/TSP-2 c |
| 45 | 496.6 | 8.6 | 1516 | 21 | AAZ21836 | Human breast and o |

ALIGNMENTS

RESULT 1

ABN95662 standard; DNA; 5784 BP.

AC ABN95662;

DT 13-AUG-2002 (first entry)

DE Gene #2160 used to diagnose liver cancer.

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
metastatic liver tumor; cytostatic; expression profile; disease state;
disease progression; drug toxicity; drug efficacy; drug metabolism.

OS Homo sapiens.

PN WO200229103-A2.

PD 11-APR-2002.

PF 02-OCT-2001; 2001WO-US30589.

PR 02-OCT-2000; 2000US-237054P.

PA (GENE-) GENE LOGIC INC.

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

DR WPI; 2002-426119/45.

PT Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient,

PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample

XX Claim 1; SEQ ID NO 2160; 298pp; English.

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 other;

Query Match 100.0%; Score 5784; DB 24; Length 5784;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGCATCCAGTACAGAGGGGTGACCTTGGACCCCTCAGCAGCCCTGCACAGGAGAAG 60
DB 1 ACGGCATCCAGTACAGAGGGGTGACCTTGGACCCCTCAGCAGCCCTGCACAGGAGAAG 60
QY 61 CGGCATATAAGCCCGCTGCCGGAGCCGCTCGGCCAGCTCCACCGAGCATCCTGCA 120
DB 61 CGGCATATAAGCCCGCTGCCGGAGCCGCTCGGCCAGCTCCACCGAGCATCCTGCA 120
QY 121 CTGACGGCCGCTCTCGCTCCAGCAGCCTCGCCCTTTCTGACTCGGTCCGGAACAC 180
DB 121 CTGACGGCCGCTCTCGCTCCAGCAGCCTCGCCCTTTCTGACTCGGTCCGGAACAC 180
QY 181 TGAAACAGTATCATCTGCATCTTTTGGCAAAACAGGAGCTCAGCTCGAGGAGCAGGA 240
DB 181 TGAAACAGTATCATCTGCATCTTTTGGCAAAACAGGAGCTCAGCTCGAGGAGCAGGA 240
QY 241 TGGTCTGAGAGCTGCTCTGCTGCTGCTGGGTGTCGCCAGCAGCAGCAAGCTGCTACC 300
DB 241 TGGTCTGAGAGCTGCTCTGCTGCTGCTGGGTGTCGCCAGCAGCAGCAAGCTGCTACC 300
QY 301 AGGACAAAGACAGACCTTCGACCTTTTTCAGTATCAGCAACATCAACCGCAAGACATTG 360
DB 301 AGGACAAAGACAGACCTTCGACCTTTTTCAGTATCAGCAACATCAACCGCAAGACATTG 360
QY 361 CGCCCAAGCAGTTCCGGGGCCGACCCCGCTGCCGCTTACCGCTTCGTCGGCTTTG 420
DB 361 CGCCCAAGCAGTTCCGGGGCCGACCCCGCTGCCGCTTACCGCTTCGTCGGCTTTG 420
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DB 421 ACTATATCCACCGGTGAACCGAGATGACCTCAGCAAGATCAACAGATATGCGGAGCA 480
QY 481 AGGAGGGCTTCTCTCTACAGCCCGCAGCTCAAGCAGGAGCGCAAGTCCAGGGGCGAGCTGT 540
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QY 781 AGCAGCTTGACGCGGAAAAGAGCCGGATGTAGTGGCCAAAGGCTCTGCCAGAGAGTTC 840
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DB 1021 GGAGCCCGAGGTGGCCAGCAAGCTCGTGGAGGAGCTGGAAACATGCTCCAGGAGCTCT 1080
QY 1081 CGGGCTCCAGCTCTCGTGAACAGCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATA 1140
DB 1081 CGGGCTCCAGCTCTCGTGAACAGCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATA 1140
QY 1141 ACCAGTTCTCTGGAGCTCATTTGGTGGCCCTCTTAAGCAAGAACATGTCAGCTTGT 1200
DB 1141 ACCAGTTCTCTGGAGCTCATTTGGTGGCCCTCTTAAGCAAGAACATGTCAGCTTGT 1200
QY 1201 GGCAGGATGGCCGCTTCTTGGGAAATGAACGTTGGTGGTGGTGGTGGTGGTGGTGGT 1260
DB 1201 GGCAGGATGGCCGCTTCTTGGGAAATGAACGTTGGTGGTGGTGGTGGTGGTGGTGGT 1260
QY 1261 GTACCTGCAAGAAATTTAAACCAATTTGCCACCAATCACCTGCCCGCTGCAACCTGG 1320
DB 1261 GTACCTGCAAGAAATTTAAACCAATTTGCCACCAATCACCTGCCCGCTGCAACCTGG 1320
QY 1321 CCAGTCCATCTTGTGGAGGCAATGCTGCCCTTCTGCTTCTGCTTCTGCTGCTGCTGCTG 1380
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QY 1381 AGGAGGCTGCTTCCGTTGGCAGAGTGGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1440
DB 1381 AGGAGGCTGCTTCCGTTGGCAGAGTGGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1440
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DB 1441 CCCAGCAGAGAGGGCTGCTGTGACGTCACAGCAACACCTGCTTGGGGGCTTCGATCC 1500
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DB 1741 CCCGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800

XX 07-FEB-2002.
 XX 31-JUL-2001; 2001WO-US24147.
 XX 01-AUG-2000; 2000US-222071P.
 XX (UNIW) UNIV WASHINGTON.
 XX Bornstein P, Kyriakides T, Ratner B, Giachelli C, Martinson L;
 XX Scatena M;
 XX WPI; 2002-217098/27.
 XX P-PSDB; AAU76902.
 XX Modulating the amount or biological activity of thrombospondin 2 or
 XX osteopontin in an animal for modulating a wound response, comprises
 XX introducing osteopontin or thrombospondin 2 antagonist into an animal -
 XX Disclosure; Page 50-54; 54pp; English.
 XX This invention relates to a method for modulating the amount or
 XX biological activity of thrombospondin 2 or osteopontin in an animal. The
 XX method involves introducing into the animal an osteopontin or
 XX thrombospondin 2 antagonist. Using the methods of the invention the
 XX amount or biological activity of thrombospondin 2 or osteopontin
 XX protein may be modulated. The method of the invention is useful for
 XX modulating the amount or biological activity of thrombospondin 2 or
 XX osteopontin in an animal which exhibits a wound response or a foreign
 XX body response, where the method can be used to improves the wound
 XX response or reduces the foreign body response. The method is
 XX useful for modulating a wound response or for reducing a foreign body
 XX response in an animal and is also useful for improving the wound
 XX response, such as at the site of a cut, abrasion or burn. The
 XX present sequence represents the human cDNA encoding the thrombospondin
 XX 2 protein used in the method of the invention.
 XX Sequence 5784 BP; 1447 A; 1460 C; 1518 G; 1359 T; 0 other;
 XX
 Query Match 100.0%; Score 5784; DB 24; Length 5784;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
ABL62660
ID ABL62660 standard; DNA; 5784 BP.
XX
AC ABL62660;
XX
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Db 2161 CGGAAAAGCAAGTGTGTGAGCCCGAAAAACCATCAAGAGCAACAGACACAACTGCCACA 2220
QY 2221 AGCAGCGGAGTGCATCTACCTGGTCACTTTCAGCGACCCCATGTACAAGTGGAGTGC 2280
Db 2221 AGCAGCGGAGTGCATCTACCTGGTCACTTTCAGCGACCCCATGTACAAGTGGAGTGC 2280
QY 2281 AGCAGGCTAGCGGGGCGAGGGGCTCATCTCGGGGGAGGACTCGGACCTGACGGCTGGC 2340
Db 2281 AGCAGGCTAGCGGGGCGAGGGGCTCATCTCGGGGGAGGACTCGGACCTGACGGCTGGC 2340
QY 2341 CCAACCTCAATCTGCTGCGCCACCAAGGCCACTTACCACTGCATCAAGATAACTGCC 2400
Db 2341 CCAACCTCAATCTGCTGCGCCACCAAGGCCACTTACCACTGCATCAAGATAACTGCC 2400
QY 2401 CCCATCTGCCAAATTTCTGGGCGAGGAAGACTTTGACAGGAGCGGATTTGGCGATGCTGTG 2460
Db 2401 CCCATCTGCCAAATTTCTGGGCGAGGAAGACTTTGACAGGAGCGGATTTGGCGATGCTGTG 2460
QY 2461 ATGATGAGGATGACAATGACGGTGTGACCGATGAGAGGAGCAACTGCCAGCTCTCTTCA 2520
Db 2461 ATGATGAGGATGACAATGACGGTGTGACCGATGAGAGGAGCAACTGCCAGCTCTCTTCA 2520
QY 2521 ATCCCCCGCAGGCTGACTATGACAAGGATGAGTTGGGACCGCTGTGACAACCTGCCCTT 2580
Db 2521 ATCCCCCGCAGGCTGACTATGACAAGGATGAGTTGGGACCGCTGTGACAACCTGCCCTT 2580
QY 2581 ACGTGCAACAACCCCTGCCAGATCGACAGACAACATGGAGAGGGTGCACCCCTGCTCCG 2640
Db 2581 ACGTGCAACAACCCCTGCCAGATCGACAGACAACATGGAGAGGGTGCACCCCTGCTCCG 2640
QY 2641 TGGACATTTGATGGGAGAGTGTCTTCAATGAACGAGACAATTTGCCCTACGCTCTACAACA 2700
Db 2641 TGGACATTTGATGGGAGAGTGTCTTCAATGAACGAGACAATTTGCCCTACGCTCTACAACA 2700
QY 2701 CTGACACAGAGGAGACACGGATGCTGACGGTGTGGGGATCACTGTGACAACCTGCCCCCTGG 2760
Db 2701 CTGACACAGAGGAGACACGGATGCTGACGGTGTGGGGATCACTGTGACAACCTGCCCCCTGG 2760
QY 2761 TGCACAACCCCTGACAGACCGCTGGACAAATGACCTTTGTTGGGAGCCAGTGTGACAACA 2820
Db 2761 TGCACAACCCCTGACAGACCGCTGGACAAATGACCTTTGTTGGGAGCCAGTGTGACAACA 2820
QY 2821 ACGAGGACATAGATGACAGCGGCCACAGACAACACGAGGAACTGCCCTTACATCTCCA 2880
Db 2821 ACGAGGACATAGATGACAGCGGCCACAGACAACACGAGGAACTGCCCTTACATCTCCA 2880
QY 2881 ACGCCAAACCCAGGCTGACCATGACAGAGACGGCCAGGCGGCTGTGACCCCTGATGATG 2940
Db 2881 ACGCCAAACCCAGGCTGACCATGACAGAGACGGCCAGGCGGCTGTGACCCCTGATGATG 2940

QY 2471 TGACAAATGACGGGTGTGACCGGATGAGAGGACAACTGCCAGCTCCTCTTCAATCCCCGCCA 2530
DB 454 TGACAAATGACGGGTGTGACCGGATGAGAGGACAACTGCCAGCTCCTCTTCAATCCCCGCCA 513
QY 2531 GCGTGACTATGACAAGGATGAGGTTGGGGACCGCTGTGACAACTGCCCTTACGTGCACAA 2590
DB 514 GCGTGACTATGACAAGGATGAGGTTGGGGACCGCTGTGACAACTGCCCTTACGTGCACAA 573
QY 2591 CCTGCCAGATCGACACAGACAACAAATGAGAGGGTGACGGCTGTCTCGTGACATTGA 2650
DB 574 CCTGCCAGATCGACACAGACAACAAATGAGAGGGTGACGGCTGTCTCGTGACATTGA 633
QY 2651 TGGGGACGATGCTTCAATGAAAGGACAAATTTGCCCTACGCTTACAACACTGACAGAG 2710
DB 634 TGGGGACGATGCTTCAATGAAAGGACAAATTTGCCCTACGCTTACAACACTGACAGAG 693
QY 2711 GGACACGGATGTGACGGGTGTGGGGATCAGTGTGACAACTGCCCTGGTGACAAACC 2770
DB 694 GGACACGGATGTGACGGGTGTGGGGATCAGTGTGACAACTGCCCTGGTGACAAACC 753
QY 2771 TGACCAGACCGAGTGGACAAATGACCTTGTGGGACCAAGTGTGACAAACAGGACAT 2830
DB 754 TGACCAGACCGAGTGGACAAATGACCTTGTGGGACCAAGTGTGACAAACAGGACAT 813
QY 2831 AGATGACGACGGCCACAGAACCAACAGGACAACTGCCCTACATCTCCAACGCCAACCA 2890
DB 814 AGATGACGACGGCCACAGAACCAACAGGACAACTGCCCTACATCTCCAACGCCAACCA 873
QY 2891 GGCTGACCATGACAGACGGCCAGGGCGACCGCTGTGACCCCTGATGATGACAAAGTGG 2950
DB 874 GGCTGACCATGACAGACGGCCAGGGCGACCGCTGTGACCCCTGATGATGACAAAGTGG 933
QY 2951 CGTCCCGATGACAGGGACAACTGCCGCTGTGTTCAACCCAGACCGAGGAGCTTGA 3010
DB 934 CGTCCCGATGACAGGGACAACTGCCGCTGTGTTCAACCCAGACCGAGGAGCTTGA 993
QY 3011 CGGTGATGGACGGGTGATATTGTTAAAGATGATTTGACAAATGACAACTCCAGATAT 3070
DB 994 CGGTGATGGACGGGTGATATTGTTAAAGATGATTTGACAAATGACAACTCCAGATAT 1053
QY 3071 TGATGATGTGTCTCTGAAAACAAATGCCATCAGTACAGACAGACTTCAGGAATCCAGAT 3130
DB 1054 TGATGATGTGTCTCTGAAAACAAATGCCATCAGTACAGACAGACTTCAGGAATCCAGAT 1113
QY 3131 GGTCCCGCTTGGATCCCAAAGGACCAACCAATTTGATCCCACTGGGTCAATTCGCCATCA 3190
DB 1114 GGTCCCGCTTGGATCCCAAAGGACCAACCAATTTGATCCCACTGGGTCAATTCGCCATCA 1173
QY 3191 AGGCAAGGAGCTGTTTCAGACAGCCAACTCGGACCCCGGCATCGCTGTAGGTTTTCAGCA 3250
DB 1174 AGGCAAGGAGCTGTTTCAGACAGCCAACTCGGACCCCGGCATCGCTGTAGGTTTTCAGCA 1233
QY 3251 GTTTGGGCTGTGGACTTCAGTGGGACATTTCTACGTAACACTGACCGGACGACGACTA 3310
DB 1234 GTTTGGGCTGTGGACTTCAGTGGGACATTTCTACGTAACACTGACCGGACGACGACTA 1293
QY 3311 TGCTGGCTTCGCTTGTGTTACAGTCAAGACGCGCTTCTATGTGGTGTGATGTGGAAGCA 3370
DB 1294 TGCCGGCTTCGCTTGTGTTACAGTCAAGACGCGCTTCTATGTGGTGTGATGTGGAAGCA 1353
QY 3371 GGTGACGACGACCTACTGGGAGGACCAACCCACGCGGCTTATGGCTACTCCGGCGTGC 3430
DB 1354 GGTGACGACGACCTACTGGGAGGACCAACCCACGCGGCTTATGGCTACTCCGGCGTGC 1413
QY 3431 CCTCAAGTGTGTAACCTCCACCGGGGACGGGCGAGCACTGAGGAACGCGCTGTGGCA 3490
DB 1414 CCTCAAGTGTGTAACCTCCACCGGGGACGGGCGAGCACTGAGGAACGCGCTGTGGCA 1473
QY 3491 CACGGGGAACACGCGGGGACGGTGCAGAACTTTATGGCAGCAGCCCGAGAACTTGGCTG 3550
DB 1474 CACGGGGAACACGCGGGGACGGTGCAGAACTTTATGGCAGCAGCCCGAGAACTTGGCTG 1533

QY 3551 GAAGGACTACAGGGCTATAGGTGGCACTAGTGGCACTACAGGCCCAAGACCGGTACATCAG 3610
DB 1534 GAAGGACTACAGGGCTATAGGTGGCACTAGTGGCACTACAGGCCCAAGACTGGCTACATCAG 1593
QY 3611 AGTCTTAGTGCATGAGGAAAACAGGTGATGGCAGACTCAGGACCTATCTATGACCAAC 3670
DB 1594 AGTCTTAGTGCATGAGGAAAACAGGTGATGGCAGACTCAGGACCTATCTATGACCAAC 1653
QY 3671 CTACGCTGCGGGCGGCTGGGTCTATTCTCTCTCAAGAAATGGTCTATTCTCTCAGA 3730
DB 1654 CTACGCTGCGGGCGGCTGGGTCTATTCTCTCTCAAGAAATGGTCTATTCTCTCAGA 1713
QY 3731 CCTCAAGTACGAATGACAGATATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTG 3790
DB 1714 CCTCAAGTACGAATGACAGATATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTG 1773
QY 3791 TGCATGCCATGCTCCCTAGACACCTCAGTTCAATTTGGTCTCTTGGGCTTCTCTCTTAG 3850
DB 1774 TGCATGCCATGCTCCCTAGACACCTCAGTTCAATTTGGTCTCTTGGGCTTCTCTCTTAG 1833
QY 3851 CAGCACCTCCTGCTCCCTTGACCTTAACCTGATGGTCTTCACTCCTGCCAGCAACCCC 3910
DB 1834 CAGCACCTCCTGCTCCCTTGACCTTAACCTGATGGTCTTCACTCCTGCCAGCAACCCC 1893
QY 3911 AAACCCAAAGTGCCTTCAGAGGATAAATATCAATGGAACCTCAGAGATGAACATTAACCCA 3970
DB 1894 AAACCCAAAGTGCCTTCAGAGGATAAATATCAATGGAACCTCAGAGATGAACATTAACCCA 1953
QY 3971 CTAGAGGAACCCAGTTGGTGATATGAGACTTTATGTGGAGTGAANAATTTGGGATGCC 4030
DB 1954 CTAGAGGAACCCAGTTGGTGATATGAGACTTTATGTGGAGTGAANAATTTGGGATGCC 2013
QY 4031 ATTACATGCTTTTCTTTGTTTAAAGAAATGAGCTTTTACATATAAATGTAATTA 4090
DB 2014 ATTACATGCTTTTCTTTGTTTAAAGAAATGAGCTTTTACATATAAATGTAATTA 2073
QY 4091 CTTATTGATTTATGTATATGAGTTGAAGGAAATACTGTGCATTAAGCCATTTATGATA 4150
DB 2074 CTTATTGATTTATGTATATGAGTTGAAGGAAATACTGTGCATTAAGCCATTTATGATA 2133
QY 4151 AATTAAAGCATGAAAATATTGCTGAACCTACTTTGGTGTCTTAAAGTTGTCACTATTCTTG 4210
DB 2134 AATTAAAGCATGAAAATATTGCTGAACCTACTTTGGTGTCTTAAAGTTGTCACTATTCTTG 2193
QY 4211 AATTAGAGTTGCTCTACAATGACACACAAATCCCGCTTAAATAATATAAACAAGGTCA 4270
DB 2194 AATTAGAGTTGCTCTACAATGACACACAAATCCCGCTTAAATAATATAAACAAGGTCA 2253
QY 4271 AATTCAATTTGAAGTAAATGTTTGTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAT 4330
DB 2254 AATTCAATTTGAAGTAAATGTTTGTAGTAAGGAGAGATTAGAAGACAACAGGCATAGCAAT 2313
QY 4331 GACATAAGCTACCGATTAACTAAATCGGAACATGTAAGACAGTTACAAAATAAAGCAACT 4390
DB 2314 GACATAAGCTACCGATTAACTAAATCGGAACATGTAAGACAGTTACAAAATAAAGCAACT 2373
QY 4391 CTCTCTTGTCTCTACAATGAAAGCCCTCATGTGCAAGTACAGATTCAGTTTCAACAGAA 4450
DB 2374 CTCTCTTGTCTCTACAATGAAAGCCCTCATGTGCAAGTACAGATTCAGTTTCAACAGAA 2433
QY 4451 CAACATCCTTGCAAATGGGTGTGACGGGTTTCCAGATGTGGATTTGGCAAAACCTCATTT 4510
DB 2434 CAACATCCTTGCAAATGGGTGTGACGGGTTTCCAGATGTGGATTTGGCAAAACCTCATTT 2493
QY 4511 TAAGTAAAGGTTAGCAGAGCAAGTGGGTGCTTTTACTGCTGCTTGTGGGTTGTGGC 4570
DB 2494 TAAGTAAAGGTTAGCAGAGCAAGTGGGTGCTTTTACTGCTGCTTGTGGGTTGTGGC 2553
QY 4571 GTCGGGAGGCTCCTGCTGAGCTTCTTCCAGCTTTTGTGCTTGTGCTGAGAGAACCCAG 4630
DB 2554 GTCGGGAGGCTCCTGCTGAGCTTCTTCCAGCTTTTGTGCTTGTGCTGAGAGAACCCAG 2613
QY 4631 CAGACGACAGGCCGGAAGGCGCATCTAACGCGTATCTAGGCTTTTGGTAACTCGGAC 4690

| CC | TSP-2 activity. | Query Match | 61.8%; | Score 3573.6; | DB 21; | Length 3596; |
|----|--|--|--------|---------------|--------|-------------------|
| XX | | Best Local Similarity | 99.6%; | Pred. No. 0; | | |
| SQ | Sequence 3596 BP; 814 A; 1051 C; 1068 G; 663 T; 0 other; | Matches 3582; Conservative | 0; | Mismatches | 14; | Indels 0; Gaps 0; |
| QY | 215 | CAGGAGCTCAGCTGCAGGAGGACGATGGTCTGGAGGCTGGTCTGCTGGCTCTGTGGGT | 274 | | | |
| DB | 1 | CAGGAGCTCAGCTGCAGGAGGACGATGGTCTGGAGGCTGGTCTGCTGGCTCTGTGGGT | 60 | | | |
| QY | 275 | GTGCCCCAGCACGCAAGCTGGTCTACAGGACAAAGACACAGACCTTTCGACCTTTTCAGTAT | 334 | | | |
| DB | 61 | GTGCCCCAGCACGCAAGCTGGTCTACAGGACAAAGACACAGACCTTTCGACCTTTTCAGTAT | 120 | | | |
| QY | 335 | CAGCAACATCAACCGCAAGACATTTGGGGCCAAAGCAGTTTCGGGGCCCGACCCCGGGCT | 394 | | | |
| DB | 121 | CAGCAACATCAACCGCAAGACATTTGGGGCCAAAGCAGTTTCGGGGCCCGACCCCGGGCT | 180 | | | |
| QY | 395 | CGCGCTTACCGCTTCGTGGCGTTTGACTACATCCACCGGTGAACGAGATGACCTCAG | 454 | | | |
| DB | 181 | CGCGCTTACCGCTTCGTGGCGTTTGACTACATCCACCGGTGAACGAGATGACCTCAG | 240 | | | |
| QY | 455 | CAAGATCACCAAGATCATCGCGCAAGAGGGCTTCTTCCTCAGCGGCCAGCTCAAGCA | 514 | | | |
| DB | 241 | CAAGATCACCAAGATCATCGCGCAAGAGGGCTTCTTCCTCAGCGGCCAGCTCAAGCA | 300 | | | |
| QY | 515 | GGAGGCAAGTCCAGGGGACGCTTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGCA | 574 | | | |
| DB | 301 | GGAGGCAAGTCCAGGGGACGCTTTGGCTCTGGAGGGCCCGGTCTCTCCAGAGGCA | 360 | | | |
| QY | 575 | GTTCCAGATCGTCTCCAACGGCCCGCGACACGCTGGATCTCACTACTCGATTGACGG | 634 | | | |
| DB | 361 | GTTCCAGATCGTCTCCAATGCCCCCGGACACGCTGGATCTCACTACTCGATTGACGG | 420 | | | |
| QY | 635 | CACCCGGCATGTGTTCCCTCGAGGAGCTCGGCTGACTGCAGTGGAGAAAGCT | 694 | | | |
| DB | 421 | CACCCGGCATGTGTTCCCTCGAGGAGCTCGGCTGACTGCAGTGGAGAAAGCT | 480 | | | |
| QY | 695 | CACCGTCAGGTGGCTGGGAGACCTACAGCTTGCACGTGGGCTCGACCTCATAGGACC | 754 | | | |
| DB | 481 | CACCGTCAGGTGGCTGGGAGACCTACAGCTTGCACGTGGGCTCGACCTCATAGACAG | 540 | | | |
| QY | 755 | AGTTGCTCTGACGAGCCCTTCTACGACACCTGCAGCGGAAAAGACCCGGATGTAGCT | 814 | | | |
| DB | 541 | CTTGCTCTGACGAGCCCTTCTAGGACACCTGCAGCGGAAAAGACCCGGATGTAGCT | 600 | | | |
| QY | 815 | GGCCAAAGGCTCTCCAGAGAGAGTCACTTCAGGGGTTTGGTTTCAGAACGTCACCTAGT | 874 | | | |
| DB | 601 | GGCCAAAGGCTCTCCAGAGAGAGTCACTTCAGGGGTTTGGTTTCAGAACGTCACCTAGT | 660 | | | |
| QY | 875 | GTTTGAACCTCTGTGAAGATATTTAAGCAAGAGGTTTCAGCAGNAGCCAGGGAGC | 934 | | | |
| DB | 661 | GTTTGAACCTCTGTGAAGATATTTAAGCAAGAGGTTTCAGCAGNAGCCAGGGAGC | 720 | | | |
| QY | 935 | TGAGATCAACGCCATCAGTGAACACAGAGACGCTGCGCCTGGTCCGATGTCACAC | 994 | | | |
| DB | 721 | TGAGATCAACGCCATCAGTGAACACAGAGACGCTGCGCCTGGTCCGATGTCACAC | 780 | | | |
| QY | 995 | CGAGTACGTGGGCCCCAGCTCGGAGAGAGGCCCGAGGTGTGCAACGCTCGTCGAGGA | 1054 | | | |
| DB | 781 | CGAGTACGTGGGCCCCAGCTCGGAGAGAGGCCCGAGGTGTGCAACGCTCGTCGAGGA | 840 | | | |
| QY | 1055 | GCTGGGAACATGTTCCAGGAGCTCTCGGGGCTCCAGTCTCTGTGAACAGCTCAGGGA | 1114 | | | |
| DB | 841 | GCTGGGAACATGTTCCAGGAGCTCTCGGGGCTCCAGTCTCTGTGAACAGCTCAGGGA | 900 | | | |
| QY | 1115 | GAACCTCAAGAGAGTGTGCAATGATAACCACTTTCTTGGGAGCTCATTTGGTGGCCCTCC | 1174 | | | |
| DB | 901 | GAACCTCAAGAGAGTGTGCAATGATAACCACTTTCTTGGGAGCTCATTTGGTGGCCCTCC | 960 | | | |
| QY | 1175 | TAAGACAAGGAACATGTACGCTTGGCAGGATGGCGGGTCTTTTCGGGAAAAATGAAC | 1234 | | | |

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|----|------|---|------|
| Db | 961 | TAAGACAAGGAACATGTCAAGTTCGCTGGCAGGATGGCCGGTTCTTTTCGGGAAAATGAAC | 1020 |
| Qy | 1235 | GTGGGTGGTGACAGCTGCACACAGCTGTACCTGCGCAGAAATTTAAACCAATTTGCCACCA | 1294 |
| Db | 1021 | GTGGGTGGTGACAGCTGCACACAGCTGTACCTGCGCAGAAATTTAAACCAATTTGCCACCA | 1080 |
| Qy | 1295 | AATCACCTGCCCGCTGCACACCTGGCCAGTCCATCTTTGTGGAAGCGAATGCTGCC | 1354 |
| Db | 1081 | AATCACCTGCCCGCTGCACACCTGGCCAGTCCATCTTTGTGGAAGCGAATGCTGCC | 1140 |
| Qy | 1355 | TTCTTGCTCCACTCGGTGGACGGTGAGAGGGCTGGTCTCCGTGGGAGAGTGGACCCA | 1414 |
| Db | 1141 | TTCTTGCTCCACTCGGTGGACGGTGAGAGGGCTGGTCTCCGTGGGAGAGTGGACCCA | 1200 |
| Qy | 1415 | GTGTCCGTGACGTGGTCTTGGACCCAGACAGAGAGGCGGTCCTGTGACGTACACAG | 1474 |
| Db | 1201 | GTGTCCGTGACGTGGTCTTGGACCCAGACAGAGAGGCGGTCCTGTGACGTACACAG | 1260 |
| Qy | 1475 | CAACACCTGCTTGGGGCCCTCGATCCAGACACGGGCTGCGAGTCTGACAAAGTGTGACAC | 1534 |
| Db | 1261 | CAACACCTGCTTGGGGCCCTCGATCCAGACACGGGCTGCGAGTCTGACAAAGTGTGACAC | 1320 |
| Qy | 1535 | CCGCATCCGGCAGGACGGCGCTGGAGCCACCTGGTCACCTTGGTCTTCACTGCTGTGAC | 1594 |
| Db | 1321 | CCGCATCCGGCAGGACGGCGCTGGAGCCACCTGGTCACCTTGGTCTTCACTGCTGTGAC | 1380 |
| Qy | 1595 | CTGTGGAGTTGGCANATACACGCATCCGTCTCTGCAACTCCCCAGTGCACATGCGG | 1654 |
| Db | 1381 | CTGTGGAGTTGGCANATACACGCATCCGTCTCTGCAACTCCCCAGTGCACATGCGG | 1440 |
| Qy | 1655 | GGGCAAGAAATTGAAAGGAGTGGCGGAGACCAAGAGCTGCCAGGGCGCCCATGCC | 1714 |
| Db | 1441 | GGGCAAGAAATTGAAAGGAGTGGCGGAGACCAAGAGCTGCCAGGGCGCCCATGCC | 1500 |
| Qy | 1715 | AATCGATGGCCCTGGAGCCCTTGGTCCCGCTGGTGGCCCTGCATGTCACTGTGCGCG | 1774 |
| Db | 1501 | AATCGATGGCCCTGGAGCCCTTGGTCCCGCTGGTGGCCCTGCATGTCACTGTGCGCG | 1560 |
| Qy | 1775 | TGGATCCGGAGGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGAGGGAAGGC | 1834 |
| Db | 1561 | TGGATCCGGAGGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGAGGGAAGGC | 1620 |
| Qy | 1835 | CTCGCTGGGGATGTGCAGAGCGTTCAGATGTCAACAGAGGAGCTGCCCCGTGGATGG | 1894 |
| Db | 1621 | CTCGCTGGGGATGTGCAGAGCGTTCAGATGTCAACAGAGGAGCTGCCCCGTGGATGG | 1580 |
| Qy | 1895 | CTGTTTATCAACCCCTTGCTTCCGGAGCCCAAGTGCAGCAGCTTCCCGATGGGTCTCGT | 1954 |
| Db | 1681 | CTGTTTATCAACCCCTTGCTTCCGGAGCCCAAGTGCAGCAGCTTCCCGATGGGTCTCGT | 1740 |
| Qy | 1955 | GTATGCGGCTTGTGCGCTGTGGGCTTCTTGGGCAATGGCACCACTGTGAGGACCTTGA | 2014 |
| Db | 1741 | GTATGCGGCTTGTGCGGCTTCTTGGGCAATGGCACCACTGTGAGGACCTTGA | 1800 |
| Qy | 2015 | CGAGTGGCCCTGGTCCCGACATCTGCTTCCACACAGCAAGTGCCTCGCTGTGCA | 2074 |
| Db | 1801 | CGAGTGGCCCTGGTCCCGACATCTGCTTCTCCACCAAGGAGTGCCTCGCTGTGCA | 1860 |
| Qy | 2075 | CACTCAGCCTGGCTTCCACTGCTTCCCTTGGCCGCCCGCCGATACAGAGGAACACGCCGT | 2134 |
| Db | 1861 | CACTCAGCCTGGCTTCCACTGCTTCCCTTGGCCGCCCGCCGATACAGAGGAACACGCCGT | 1920 |
| Qy | 2135 | CGGGGTGGCTGGAGCAGCCAGACGGGAAGCAAGTGTGTGAGCCCGAAGACCATG | 2194 |
| Db | 1921 | CGGGGTGGCTGGAGCAGCCAGACGGGAAGCAAGTGTGTGAGCCCGAAGACCATG | 1980 |
| Qy | 2195 | CAAGGACAAGACACAACCTGCCACAAGCACGCGAGTGCATCTACCTGGGTCACTTCAG | 2254 |
| Db | 1981 | CAAGGACAAGACACAACCTGCCACAAGCACGCGAGTGCATCTACCTGGGTCACTTCAG | 2040 |
| Qy | 2255 | CGACCCCATGTACAAGTGGAGTGGCAGACAGGCTTACCGGGCGACGGGTCACTTCGCG | 2314 |

CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of p by expressing
CC inactive proteins or to supplement the patients own production of p.
CC Additionally, N may be used to produce the colon cancer-associated ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and p can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB7789 represent sequences used in the exemplification of the
CC present invention.

CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 3522 BP; 970 A; 808 C; 844 G; 893 T; 7 other;

Query Match 58.9%; Score 3404.8; DB 22; Length 3522;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3444; Conservative 3; Mismatches 5; Indels 8; Gaps 3;

| | | | |
|----|------|---|------|
| QY | 2051 | CAGCAAGTGCCCTCGCTGTGTCAACACTCAGCCTGGCTTCCACTGCTGCCCTGCCCGCC | 2110 |
| DB | 34 | CAGCAAGGTGCTCGCTGTGTCAACACTCAGCCTGGCTTCCACTGCTGCCCTGCCCGCC | 93 |
| QY | 2111 | CCGATACAGAGGGAACCAAGCCGTCGGGTGCGCTGGAAGCAGCAACAGCGAAAGCA | 2170 |
| DB | 94 | CCGATACAGAGGGAACCAAGCCGTCGGGTGCGCTGGAAGCAGCAACAGCGAAAGCA | 153 |
| QY | 2171 | AGTGTGTGAGCCCGCAAAACCCATGCAAGGACAAAGACACACAACTGCCAAGCAGCGGA | 2230 |
| DB | 154 | AGTGTGTGAGCCCGCAAAACCCATGCAAGGACAAAGACACACAACTGCCAAGCAGCGGA | 213 |
| QY | 2231 | GTGCATCTACCTGGGTGCTACTTCAGCGACCCCATGTACAGTCCGAGTGCCAGACAGGCTA | 2290 |
| DB | 214 | GTGCATCTACCTGGGTGCTACTTCAGCGACCCCATGTACAGTCCGAGTGCCAGACAGGCTA | 273 |
| QY | 2291 | CSCGGGCGACGGGCTCATCTCGGGGAGGAGCTCGGACCTGGAGCGCTGCCCAACTCAA | 2350 |
| DB | 274 | CSCGGGCGACGGGCTCATCTCGGGGAGGAGCTCGGACCTGGAGCGCTGCCCAACTCAA | 333 |
| QY | 2351 | TCGTCTCTGCGCCACCAACCGCCATACCTGCACTGCAATCAAGGATACTGCCCCATCTGCC | 2410 |
| DB | 334 | TCGTCTCTGCGCCACCAACCGCCATACCTGCACTGCAATCAAGGATACTGCCCCATCTGCC | 393 |
| QY | 2411 | AAATTCCTGGCAGGAAGACTTTGACAGGACGGGATTTGGCGATGCTGTGATGATGACGA | 2470 |
| DB | 394 | AAATTCCTGGCAGGAAGACTTTGACAGGACGGGATTTGGCGATGCTGTGATGATGACGA | 453 |
| QY | 2471 | TGCAATGACGGTGTACCGATGAGAAGCAACATGCGAGCTCCCTTCAATCCCGGCCA | 2530 |
| DB | 454 | TGCAATGACGGTGTACCGATGAGAAGCAACATGCGAGCTCCCTTCAATCCCGGCCA | 513 |
| QY | 2531 | GGCTGACTATGACAAAGGATGAGTTGGGAGCCGCTGTGACAACTGCCCTTACGTGCACAA | 2590 |
| DB | 514 | GGCTGACTATGACAAAGGATGAGTTGGGAGCCGCTGTGACAACTGCCCTTACGTGCACAA | 573 |
| QY | 2591 | CCCTGCCAGATCGACACAGCAACAATGGAGAGGGTGACGGCTGCTCCGTGGACATTGA | 2650 |
| DB | 574 | CCCTGCCAGATCGACACAGCAACAATGGAGAGGGTGACGGCTGCTCCGTGGACATTGA | 633 |
| QY | 2651 | TGGGACCATGTCTTCAATGAACGAGACAATTTGCCCTACGCTCTACAACTGACCCAG | 2710 |
| DB | 634 | TGGGACCATGTCTTCAATGAACGAGACAATTTGCCCTACGCTCTACAACTGACCCAG | 693 |
| QY | 2711 | GGACACGGATGGTACGGTGTGGGGATCACTGTGACAACTGCCCTTGGTGCAACACC | 2770 |
| DB | 694 | GGACACGGATGGTACGGTGTGGGGATCACTGTGACAACTGCCCTTGGTGCAACACC | 753 |
| QY | 2771 | TGACACAGCAGCTGGACAATGACCTTTGGGGACCAAGTGTGACAAACAGAGGACAT | 2830 |
| DB | 754 | TGACACAGCAGCTGGACAATGACCTTTGGGGACCAAGTGTGACAAACAGAGGACAT | 813 |
| QY | 2831 | AGATGACACGGCCACAGCAACACAGCAACTGCCCTTACATCTCCACAGCCACCA | 2890 |

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|----|------|--|------|
| DB | 814 | AGATGACGAGCGGCCACCAAGAACCAACAGGACAACTGCCCTTACATCTCCAAAGCCCAACA | 873 |
| QY | 2891 | GGCTGACCATGACAGAGACGGCCAGGGGACCCCTGTGACCTGATGATGACAAAGATGG | 2950 |
| DB | 874 | GGCTGACCATGACAGAGACGGCCAGGGGACCCCTGTGACCTGATGATGACAAAGATGG | 933 |
| QY | 2951 | CCTCCCCGATGACAGGGCAACTGCCGGCTGTGTTCACCCAGACCCAGGAGGACTTGA | 3010 |
| DB | 934 | CCTCCCCGATGACAGGGCAACTGCCGGCTGTGTTCACCCAGACCCAGGAGGACTTGA | 993 |
| QY | 3011 | CGGTGATGACGGGGTGATATTTGTAAGATGATTTTGACATGACACATCCAGATAT | 3070 |
| DB | 994 | CGGTGATGACGGGGTGATATTTGTAAGATGATTTTGACATGACACATCCAGATAT | 1053 |
| QY | 3071 | TGATGATGTGTCTCTGAAACAATGCCATCAGTGAGACAGACTTCAGGAACCTCCAGAT | 3130 |
| DB | 1054 | TGATGATGTGTCTCTGAAACAATGCCATCAGTGAGACAGACTTCAGGAACCTCCAGAT | 1113 |
| QY | 3131 | GGTCCCTTTGGATCCCAAGGACCAACCAATTCATCCCACTGGGTCTATTCGCCATCA | 3190 |
| DB | 1114 | GGTCCCTTTGGATCCCAAGGACCAACCAATTCATCCCACTGGGTCTATTCGCCATCA | 1173 |
| QY | 3191 | AGGCAAGAGCTGTTCAGACAGCAACTCGGACCCCGCATCGCTGTAGTTTTCAGCA | 3250 |
| DB | 1174 | AGGCAAGAGCTGTTCAGACAGCAACTCGGACCCCGCATCGCTGTAGTTTTCAGCA | 1233 |
| QY | 3251 | GTTCGGGTCTGTGGACTTCAGTGGGCACATCTTACCTAAACACTGACCGGAGCAGACTA | 3310 |
| DB | 1234 | GTTCGGGTCTGTGGACTTCAGTGGGCACATCTTACCTAAACACTGACCGGAGCAGACTA | 1293 |
| QY | 3311 | TGCTGGCTTGTCTTTGGTTTACCAGTCAAGCAGCCGCTTCTATGTGGTGTATGGAAGCA | 3370 |
| DB | 1294 | TGCTGGCTTGTCTTTGGTTTACCAGTCAAGCAGCCGCTTCTATGTGGTGTATGGAAGCA | 1353 |
| QY | 3371 | GGTGACGACAGACTTACTGGAGGACCCACCGCGGCGCTATGCTACTCGGGGCTGC | 3430 |
| DB | 1354 | GGTGACGACAGACTTACTGGAGGACCCACCGCGGCGCTATGCTACTCGGGGCTGC | 1413 |
| QY | 3431 | CCTCAAGTGTGTAACTCCACACGGGACGGGCGGACCTGAGGAACGGCTGTGGCA | 3490 |
| DB | 1414 | CCTCAAGTGTGTAACTCCACACGGGACGGGCGGACCTGAGGAACGGCTGTGGCA | 1473 |
| QY | 3491 | CACGGGAAACAGCGGGGCGAGTGGCAACCTTATGGCAGCACCCAGCAATTTGGCTG | 3550 |
| DB | 1474 | CACGGGAAACAGCGGGGCGAGTGGCAACCTTATGGCAGCACCCAGCAATTTGGCTG | 1533 |
| QY | 3551 | GAAGGACTACAGCGCTATAGTGTGACCTGACTCAGAGGCGCCAGCCGCTACATCAG | 3610 |
| DB | 1534 | GAAGGACTACAGCGCTATAGTGTGACCTGACTCAGAGGCGCCAGCCGCTACATCAG | 1593 |
| QY | 3611 | AGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACTCAGGACCTATCTATGACCAAC | 3670 |
| DB | 1594 | AGTCTTAGTGCATGAAGGAAACAGGTCTATGGCAGACTCAGGACCTATCTATGACCAAC | 1653 |
| QY | 3671 | CTAGCTGGCGGGGGCTGGGTCTATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGA | 3730 |
| DB | 1654 | CTAGCTGGCGGGGGCTGGGTCTATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGA | 1713 |
| QY | 3731 | CCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTTCTCATTTCCGGCAATGCCCTG | 3790 |
| DB | 1714 | CCTCAAGTACGAATGCAGAGATATTTAAACAAGATTTTCTCATTTCCGGCAATGCCCTG | 1773 |
| QY | 3791 | TGCTAGCATGGTCCCTAGACACCTCAGTTCATTTGTGTCTTGGCTCTCTCTCTAG | 3850 |
| DB | 1774 | TGCTAGCATGGTCCCTAGACACCTCAGTTCATTTGTGTCTTGGCTCTCTCTCTAG | 1833 |
| QY | 3851 | CAGACCT | 3910 |
| DB | 1834 | CAGACCT | 1893 |
| QY | 3911 | AAACCCAGTCCCTTCAGAGGATTAATCAATGAAGTCAAGATGAACATCTAAACCCA | 3970 |
| DB | 1894 | AAACCCAGTCCCTTCAGAGGATTAATCAATGAAGTCAAGATGAACATCTAAACCCA | 1953 |

| | | | |
|----|------|---|------|
| Qy | 3971 | CTAGAGAAACCAGTTTGGTGATATATGAGACTTTATGTGGAGTGAATAATTTGGCATGCC | 4030 |
| Db | 1954 | CTAGAGAAACCAGTTTGGTGATATATGAGACTTTATGTGGAGTGAATAATTTGGCATGCC | 2013 |
| Qy | 4031 | ATTACATTCGCTTTTCTGTTGTTTAAAGAAATGACGTTTACATATATAAATGTAATTA | 4090 |
| Db | 2014 | ATTACATTCGCTTTTCTGTTGTTTAAAGAAATGACGTTTACATATATAAATGTAATTA | 2073 |
| Qy | 4091 | CTTATTGTAATTATGTGTATATGGAGTCTGAAGGGAATACTGTGCATGAAGCCATTATGATA | 4150 |
| Db | 2074 | CTTATTGTAATTATGTGTATATGGAGTCTGAAGGGAATACTGTGCATGAAGCCATTATGATA | 2133 |
| Qy | 4151 | AATTAAGCATGAATAATATGCTGAACTACTTTTGGTGCTTAAAGTTGTCACTATCTTG | 4210 |
| Db | 2134 | AATTAAGCATGAATAATATGCTGAACTACTTTTGGTGCTTAAAGTTGTCACTATCTTG | 2193 |
| Qy | 4211 | AATTAGAGTTGCTCTACAATGACACACAATCCCGCTAAATAAATTATAACAAGGTCGA | 4270 |
| Db | 2194 | AATTAGAGTTGCTCTACAATGACACACAATCCCGCTAAATAAATTATAACAAGGTCGA | 2253 |
| Qy | 4271 | ATTCAAAATTTGAAGTAATGTTTATGTAAGGACAGATTAGAAGACAACAGCATAGCAAAAT | 4330 |
| Db | 2254 | ATTCAAAATTTGAAGTAATGTTTATGTAAGGACAGATTAGAAGACAACAGCATAGCAAAAT | 2313 |
| Qy | 4331 | GACATAAGCTTACCAGATAACTAATCGGAACATGTAAAAACAGTTACAAAAATAAACGAAC | 4390 |
| Db | 2314 | GACATAAGCTTACCAGATAACTAATCGGAACATGTAAAAACAGTTACAAAAATAAACGAAC | 2373 |
| Qy | 4391 | CTCCTCTGTGCTTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTTCATCAAAAGAA | 4450 |
| Db | 2374 | CTCCTCTGTGCTTACAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTTTCATCAAAAGAA | 2433 |
| Qy | 4451 | CAACATCCTTTGCAATGGGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTT | 4510 |
| Db | 2434 | CAACATCCTTTGCAATGGGTGTGACGCGGTTCCAGATGTGGATTTGGCAAAACCTCATTT | 2493 |
| Qy | 4511 | TAAGTAAAGGTTTAGCAGACAAAGTGCGGTGCTTTAGCTGCTGCTGTGCGGTTGTGGC | 4570 |
| Db | 2494 | TAAGTAAAGGTTTAGCAGACAAAGTGCGGTGCTTTAGCTGCTGCTGTGCGGTTGTGGC | 2553 |
| Qy | 4571 | GTGGGGAGGCTCCTGCCTGAGCTTCCCTCCCGAGCTTTGCTGCTGAGAGGAACACAGAG | 4630 |
| Db | 2554 | GTGGGGAGGCTCCTGCCTGAGCTTCCCTCCCGAGCTTTGCTGCTGAGAGGAACACAGAG | 2613 |
| Qy | 4631 | CAGACGCACAGCGCGGAAAAAGGCGCATCTAACGCGTATCTAGGCTTTGGTTAACTGCGGAC | 4690 |
| Db | 2614 | CAGACGCACAGCGCGGAAAAAGGCGCATCTAACGCGTATCTAGGCTTTGGTTAACTGCGGAC | 2673 |
| Qy | 4691 | AAAGTTGCTTTTACCTGATTTGATGATACATTTCAATTAAGGTTCCAGTTTATAAATATTTTG | 4750 |
| Db | 2674 | AAAGTTGCTTTTACCTGATTTGATGATACATTTCAATTAAGGTTCCAGTTTATAAATATTTTG | 2733 |
| Qy | 4751 | TTAATATTATTAAAGTGACTATAGAAATGCAACTCCCATTTACCAGTAACTATTTTAAATA | 4810 |
| Db | 2734 | TTAATATTATTAAAGTGACTATAGAAATGCAACTCCCATTTACCAGTAACTATTTTAAATA | 2793 |
| Qy | 4811 | TGCGTAGTACACATATGTAGTATATAATTCTCTAGAAACAAACATCTAATATAGTATATAATC | 4870 |
| Db | 2794 | TGCGTAGTACACATATGTAGTATATAATTCTCTAGAAACAAACATCTAATATAGTATATAATC | 2853 |
| Qy | 4871 | CTGTGAAATATCAGGCTTGATAAATATTAGGTTGTCCAGATGACAGCATGCTAGAACGCTG | 4930 |
| Db | 2854 | CTGTGAAATATCAGGCTTGATAAATATTAGGTTGTCCAGATGACAGCATGCTAGAACGCTG | 2913 |
| Qy | 4931 | AACAGATACATAGAGAAATAATGAGAGGTTTATGATGGAACCTTAAATATATAATGTTGCC | 4990 |
| Db | 2914 | AACAGATACATAGAGAAATAATGAGAGGTTTATGATGGAACCTTAAATATATAATGTTGCC | 2973 |
| Qy | 4991 | AGCGATTTAGTTCAATATTTGTTACTGTTATCTATCTATCTGCTGATATGGAATCTCTTTAA | 5050 |
| Db | 2974 | AGCGATTTAGTTCAATATTTGTTACTGTTATCTATCTATCTGCTGATATGGAATCTCTTTAA | 3033 |

| | | | |
|--------------------------|--|--|------|
| QY | 5051 | TTCAACGCTGAATAAGAAATCAGCATTTAGTCTTGCCAGGCACACCACCAATTAATCAGTCAT | 5111 |
| Db | 3034 | TTCAAACGCTGAATAAGAAATCAGCATTTAGTCTTGCCAGGCACACCACCAATTAATCAGTCAT | 3093 |
| QY | 5111 | GTGTAATATGCACAAGTTCTGTTTTCTGTTTTTGTGTTTTTTGGTGTG---GTTTTTTT | 5166 |
| Db | 3094 | GTGTAATATGCACANGTTTGTTTTGTTTTTGTGTTTTTTGGTGTGTTTTTTGTTTTT | 3153 |
| QY | 5167 | GCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCACATCATCCCACCCACATAAGGGG | 5226 |
| Db | 3154 | GCTTTAAGTTGCATGATCTTTCTGCAGGAAATAGTCACATCATCCCACCCACATAAGGGG | 3213 |
| QY | 5227 | TTTAGTAAGAAGAGTCTGCTGCTGTCATGATGATGATAGGGGGCAAATCTTTTTCCCGCTTC | 5286 |
| Db | 3214 | TTTAGTAAGAAGAGTCTGCTGCTGTCATGATGATGATAGGGGGCAAATCTTTTTCCCGCTTC | 3273 |
| QY | 5287 | TGTTAATAGTCATCACATTTCTATGCCAACAGGAACGATCCATACCTTAGTCTTAATG | 5346 |
| Db | 3274 | TGTTAATAGTCATCACATTTCTATGCCAACAGGAACGATCCATACCTTAGTCTTAATG | 3333 |
| QY | 5347 | TACACATTGTCATTTTGATAAAAATAATTTGTTTGTGTTTCCCTTTGAGGTTGATCGTTG--T | 5403 |
| Db | 3334 | TACACATTGTCATTTTGATAAAAATAATTTGTTTGTGTTTCCCTTTGAGGTTGATCGTTG | 3393 |
| QY | 5404 | GTTGTTTGTGTCACATTTTTFACTTTTTTCGRTGTGGAGCTGTATTCGCCGAGA-CAACGAA | 5462 |
| Db | 3394 | GTTGTTTGTGTCACATTTTTFACTTTTTTCGRTGTGGAGCTGTATTCGCCGAGACCAACGAA | 3453 |
| QY | 5463 | CGGTTGGGATACTTCATTAATGTACGGACTGTCAACAGC | 5502 |
| Db | 3454 | CGGTTGGGATACTTCATTAATGTACGGACTGTCAACAGC | 3493 |
| RESULT 7 AAZ32016 | | | |
| ID | AAZ32016 | standard; DNA; 4108 BP. | |
| XX | AC | AAZ32016; | |
| XX | DT | 10-JAN-2000 (first entry) | |
| XX | DE | Human METH1 related EST L07803. | |
| XX | KW | Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss. | |
| OS | XX | Homo sapiens. | |
| PN | XX | WO9937660-A1. | |
| PD | XX | 29-JUL-1999. | |
| PF | XX | 22-JAN-1999; 99WO-US01313. | |
| PR | XX | 23-JAN-1998; 98US-0072298. | |
| PR | XX | 28-AUG-1998; 98US-0098539. | |
| PA | (IRUE/) IRUELA-ARISPE L. | | |
| PA | (HABE/) HASTINGS G A. | | |
| PA | (RUBE/) RUBEN S M. | | |
| PI | Iruela-Arispe L, Hastings GA, Ruben SM; | | |
| DR | WPI; 1999-590684/50. | | |
| PT | New isolated metalloprotease thrombospondin polypeptides, useful for | | |
| PT | treating hyperproliferative disorders, cancers or autoimmune disorders | | |
| PT | - | | |

PS Disclosure: Page 288-291; 457pp; English.

XX AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human
CC metalloproteinase thrombospondin (METH) proteins METH1 and METH2
CC respectively. METH1 and METH2 have been found to be potent inhibitors of
CC angiogenesis both in vitro and in vivo. They can be used for treating
CC cancer and other disorders related to angiogenesis including abnormal
CC wound healing, inflammation, rheumatoid arthritis, psoriasis,
CC endometrial bleeding disorders, diabetic retinopathy, some forms of
CC macula degeneration, haemangiomas, and arterial-venous malformations.
CC They may be useful in treating deficiencies or disorders of the immune
CC system, by activating or inhibiting the proliferation, differentiation,
CC or mobilization (chemotaxis) of immune cells. The etiology of these
CC immune deficiencies or disorders may be genetic, somatic, such as
CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
CC toxins), or infectious. They can also be used to treat inflammatory
CC conditions, both chronic and acute conditions. The products can also be
CC used for detection and diagnosis. AA232002 to AA232080, and AAY49503 to
CC AAY49511 represent sequences given in the exemplification of the present
CC invention.

XX SQ Sequence 4108 BP; 1033 A; 1056 C; 1110 G; 909 T; 0 other;

Query Match 47.5%; Score 2745.2; DB 20; Length 4108;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 3218; Conservative 0; Mismatches 673; Indels 9; Gaps 6;

QY 226 CTGCAGGAGGAGGATGCTCTGGAGGCTGGTCTGCTGGCTCTGGGTGGGCCAGCA 285
DB 205 CAGGTGGAGACAAGATGCTCTGGGCACTGGCCCTGCTGGCTGGGCGATAGGCCAAG 264
QY 286 CGCAAGCTGGTCCACGAGCAAGACAGCAGCTTCGACCTTTTCAGTATCAGCAACATCA 345
DB 265 CTCTTCTGGTGGTACACACCTCAAGGACACTTTCATTTGACCTTTTCAGCATCAGCAACATTA 324
QY 346 ACCGCAAGACCATTTGGCCCAAGCAGTTCGCGGCCGACCGCGCTGGCGCTTACC 405
DB 325 ACCGGAACCATCTGGTCCCAAGCAGTTCGAGGGCCCTGACCCCGGGTGGCCGCTACC 384
QY 406 GCTTGTGCGGCTTTGACTACATCCACCGGTGAACGCGAGATGACCTCAGCAAGATCA 465
DB 385 GTTTTGTACGGTTTGAATACATCCCGCCAGTGAACACAGATGATCTCAACAGGATTGCA 444
QY 466 AGATCATCGGCGAGAGGAGGCTCTCTCCACGCGCCCACTCAGCAGAGCGGCAAGT 525
DB 445 AGCTTGAAGGAGAAAGAGGGCTTCTTCTCCACAGCCCAACTGAAGCAGGACCGCAAGT 504
QY 526 CCAGGGGACGCTGTTGGCTCTCGAGGGCCCGGCTCTCCAGAGGCGAGTTCGAGATCG 585
DB 505 CTCGGGGAACGCTCCTGTGTGGAAGGCCCGGCACTCCCGAGGCGAGTTTGAGATTG 564
QY 586 TCTCCAAAGCCCGCGGACACGCTGGATCTCACCCTACTGGATTGACGGCACCGGCAATG 645
DB 565 TGTCCAAATGGCCCGAGGAGACACTTTGGACCTCAACTACTGGTAGAGGCAATCAGCATA 624
QY 646 TGGTCTCCCTGGAGGAGCTCGGCTGGCTGACTCGAGTGAAGAACGTCACCGTGCAGG 705
DB 625 CCAACTTCTCTGGAGGATGTGGGCGCTGGCTGACTCCCACTGGAAGAAATGTGACTGTG 684
QY 706 TGGTGGGAGACCTACAGCTTTCAGCTGGGCTGCGACCTCATAGGACCACTTCTCTGG 765
DB 685 TGGCCAGTGACACCTATAGCCTGTATGTGGGCTGCGATCTTATCGACAGTGTACCCCTGG 744
QY 766 ACAGGCCCTTCTACGAGCACCCTGACGCGGAAAGAGCGGATGATGTGGCCCAAGGCT 825
DB 745 AAGAACCATTCTATGACGAGCTAGAAAGTAGACAGGAGCAGGATGACGTGSCCAAGGTG 804
QY 826 CTGCAGAGAGAGTCACTTACAGGGTTTTCCTTCAGACGTCACCGTCTAGTTTGAAGACT 885
DB 805 CATCTCAGAGAGTCACTTACAGGGCTTGTGCGAAGATGCTCATCTGCTGTGTTGCAATT 864
QY 886 CTGTGGGAAGATATTCTAAGCAAGAAGGCTTGCCAGCAGGCGGAGGAGCTGAGATCAACG 945
DB 945

DB 865 CTGTGGGAAGATATCTTAAGCAAGAAAAGCTGTCAACACAGCCAGGGAGCTGAAGTCAACA 924
QY 946 CCATCAGTGAACAACACAGAGACGCTGCGCCCTGGGTCCGCATGTCAACACCGAGTACGTGG 1005
DB 925 CCATCAGTGAACAATACAGAGACTCTCCATCTGAGCCCTCACATCACACAGATCTCGTGG 984
QY 1006 GCCCAGCTCGGAGAGGAGGCCGAGGTGTGGGAACGCTCTGTGCGAGAGCTGGGAACA 1065
DB 985 TCCAGGCTGTGGGAAGGCACAGGAGGTGTGTACGCACTCTCTGCGAGGAGTTGAGCAACA 1044
QY 1066 TGGTCCAGGAGCTCTCGGGGCTCCACGTCCTCGTGAACACAGCTCAGCAGACCTCAAGA 1125
DB 1045 TGATGAATGAGCTCTCTGCACTGCACTGCTGAGTGAACAGCTGAGCAAGAACCTGGAGA 1104
QY 1126 GAGTGTCAATATCAATCAACAGTCTTCTGCGAGCTCATTTGGTGGCCCTCCTTAAGACAAGA 1185
DB 1105 GAGTGTCTAGTGAATAACCAAGTCTCTTTTGGAGCTCATTTGGGGGCCCTCTGAAGACAAGA 1164
QY 1186 ACATGTACGCTTGTGCGAGGATGCCGGTCTTTTTCGGGAAATGAACGCTGGGTGGTGG 1245
DB 1165 ACATGTACGCTTGTGCGAGGAGGCCGAATCTTTGACAGAAAATCAAAACCTGGGTGGTGG 1224
QY 1246 ACAGCTGACACAGCTGTACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACTGCC 1305
DB 1225 ATAGTTGTACCACTGCACTGCAAGAAATTTAAACAGTCTGCCATCAGATCACTGCT 1284
QY 1306 CGCTGCAACCTCGGCCAGTCCATCTCTTTGGAAGGCGAATGTGCGCTTCTCTGCCCTCC 1365
DB 1285 CACCTGCAACTTGTGCCAACCCATCTTTTGGGAAGGCGAGTGTCTCATCTCTGTTTCCAC 1344
QY 1366 ACTCGGTGGAGCTGTGAGGAGGCTGGTCTCGTGGGCAAGTGGACCACTGCTCGGTGA 1425
DB 1345 ACTCTGACAGACAGTGTGAGGCTGGTCTCGTGGGCAAGTGGACCACTGCTCTGTCA 1404
QY 1426 CGTGTGGCTCTGGGACCCAGCAGAGAGCCGCTCTGTGAGTGTCAACAGCAACCTGCC 1485
DB 1405 CTTGTGGCTCTGGGACCCAGCAGAGAGCCGCTCTGTGATGTCAACAGCAACCTGCC 1464
QY 1486 TGGGGCCCTCGATCCAGACACGCGCTTGCAGCTGAGCAAGTGTGACACCGCAGTCCGGC 1545
DB 1465 TGGGCCCTTCCATTTCAGACAAGGACATGCACTGCGCAATGTGATACGAGATCCGCTC 1524
QY 1546 AGGAGCGGCTGTGAGGACCTGCTACCTTGGTCTTCACTGTCTGTGACCTGTGAGATTG 1605
DB 1525 AGAATGAGGCTGTGAGTCACTGGTCACTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 1584
QY 1606 GCAATATCACACGATCCGCTCTGCAACTCCCGAGTCCCGCAGATGGGGGCAAGAAAT 1665
DB 1585 GCAATGTACCCGCTAGCTCTGCAACTCAGGAGTCCCGCAGATGGGTGGCAGAACT 1644
QY 1666 GCAAGGAGTGGCGGAGACCAAGGCTGCCAGGCGCCCATGCCCAATCGATGGCC 1725
DB 1645 GCAAGGCGAGGCGCGGAAACCAACCTCTGACGCTGATCCGCTGCCCAATGATGGCC 1704
QY 1726 GCTGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1785
DB 1705 GCTGAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1764
QY 1786 AGCCACCGGCTGTGCAACAGCCCTGAGCCTCAGTACGAGGAGGAGGAGGAGGAGGAGG 1845
DB 1765 AGCCCTCAGCTGTGCAACAGCCCTGAGCCCACTGAGGAGGAGGAGGAGGAGGAGGAGG 1824
QY 1846 ATGTGAGGAGGCTGAGATGTGAACAAGAGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1905
DB 1825 ATGTGACAGAACCAAAATGTGAACAAGAGAACTGCCCTATTGATGGGTGCTTATCCA 1884
QY 1906 ACCCTGCTTCCCGGAGCCGAGCTGAGAGCTTCCCGGATGGGTCTCTGCTGCTGCTGCTGCTG 1965
DB 1885 ACCGCTGCTTCCCTGAGGCAAGTGAACAGCTTCCCTGATGGGTCTCTGCTGCTGCTGCTGCTG 1944
QY 1966 TCTG 2025
DB 1945 CTTGCCAGTGGGCTTCTTGGGCAATGGTACCCACTGTGAGGAGGAGGAGGAGGAGGAGGAGG 2004

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|-----------------------|--|--|
| AC | AAC90073; | |
| XX | | |
| DT | 19-MAR-2001 (first entry) | |
| XX | | |
| DE | L07803 cDNA clone. | |
| XX | | |
| KW | METH; metalloprotease; thrombospondin; angiogenesis inhibition; | |
| KW | cancer therapy; benign tumour; ocular angiogenic disease; | |
| KW | rheumatoid arthritis; psoriasis; wound healing; endometriosis; | |
| KW | vasculogenesis; granulation; hypertrophic scar; nonunion fracture; | |
| KW | scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; | |
| KW | coronary collateral; cerebral collateral; arteriovenous malformation; | |
| KW | ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation; | |
| KW | plaque neovascularisation; telangiectasia; haemophilic joint; EST; | |
| KW | angiofibroma; fibromuscular dysplasia; expressed sequence tag; | |
| KW | Crohn's disease; atherosclerosis; birth control; ss. | |
| XX | | |
| OS | Unidentified. | |
| XX | | |
| PN | WO200071577-Al. | |
| XX | | |
| PD | 30-NOV-2000. | |
| XX | | |
| PF | 25-MAY-2000; 2000WO-US14462. | |
| XX | | |
| PR | 25-MAY-1999; 99US-0318208. | |
| PR | 20-JUL-1999; 99US-0144882. | |
| PR | 10-AUG-1999; 99US-0147823. | |
| PR | 13-AUG-1999; 99US-0373658. | |
| PR | 22-DEC-1999; 99US-0171503. | |
| XX | 22-FEB-2000; 2000US-0183792. | |
| XX | (HUMA-) HUMAN GENOME SCI INC. | |
| PA | (SMIK) SMITHKLINE BEECHAM CORP. | |
| PA | (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT. | |
| PA | (IRUE/) IRUELA-ARISPE L. | |
| PA | (HAST/) HASTINGS G A. | |
| PA | (RUBE/) RUBEN S M. | |
| PA | (JONA/) JONAK Z L. | |
| PA | (TRUL/) TRULLI S H. | |
| PA | (FORN/) FORNWALD J A. | |
| PA | (TERR/) TERRETT J A. | |
| PI | Iruela-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH; | |
| PI | Fornwald JA, Terrett JA; | |
| XX | | |
| DR | WPI; 2001-025136/03. | |
| XX | | |
| PT | METH1 and METH2 polynucleotides and encoded polypeptides, used to | |
| PT | Inhibit angiogenesis in the treatment of disorders such as cancer, | |
| PT | rheumatoid arthritis and psoriasis - | |
| XX | | |
| PS | Claim 7; Pages 589-591; 768pp; English. | |
| XX | | |
| CC | The present invention relates to human METH1 and METH2, (ME for | |
| CC | metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). | |
| CC | The present sequence is an expressed sequence tag (EST) for METH. METH | |
| CC | can be used for inhibiting angiogenesis in an individual, and for | |
| CC | treating cancer, benign tumours, an ocular angiogenic disease, | |
| CC | rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, | |
| CC | vasculogenesis, granulations, hypertrophic scars, nonunion fractures, | |
| CC | scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, | |
| CC | coronary collaterals, cerebral collaterals, arteriovenous malformations, | |
| CC | ischaemic limb angiogenesis, Osler-Webber syndrome, plaque | |
| CC | neovascularisation, telangiectasia, haemophilic joints, angiofibroma, | |
| CC | fibromuscular dysplasia, wound granulation, Crohn's disease or | |
| CC | atherosclerosis. METH can also be used in birth control. METH can also | |
| CC | be used in diagnostic methods for the prognosis of cancer. | |
| XX | | |
| SQ | Sequence 4108 BP; 1033 A; 1056 C; 1110 G; 909 T; 0 other; | |
| | | |
| Query Match | 47.5%; Score 2745.2; DB 22; Length 4108; | |
| Best Local Similarity | 82.5%; Pred. No. 0; | |

| | | | | |
|-----------------------|-------|---------------|--------|--------------|
| Query Match | 47.5% | Score 2745.2; | DB 22; | Length 4108; |
| Best Local Similarity | 82.5% | Pred. No. 0; | | |

[illegible]

Db 861 GAAGATATTCTAAGCAAGAAAGGCTGTCAACACAGCCAGGAGCTGAAGTCAACACCATC 920
Qy 951 AGTGAGAACACAGAGACCTCGCGCTGGTCCGATGTCACCAACCGAGTACGTGGGCCCC 1010
Db 921 AGTGAACATACAGAGACATCCACTGAGCCCTCACATCACACAGATCTGGTGGTCCAG 980
Qy 1011 AGCTCGGAGAGAGCCCGAGGTGTGGAAAGCTGCTCGGAGGAGCTGGGAACATGGTC 1070
Db 981 GGTGTGAGAAGGCACAGAGAGTGTGTACGCACCTCCTGTGAAGAGCTGAGCAACATGATG 1040
Qy 1071 CAGGAGCTCTCGGGCTCCACGCTCCTGTGAACACAGTGTACGCGAGAACCTCAAGAGAGTG 1130
Db 1041 AACGAGCTGTCTGGATGTCAGCTCATGTGTGAACACAGTGTGACAGAACCTGGAGAGAGTG 1100
Qy 1131 TCGAATGATTAACAGTGTCTCTGGGAGCTCAATGGTGGCCCTCTTAAGACAAGAAACATG 1190
Db 1101 TCTAGCGATAAACAGTGTCTTTTGGAGCTCATCGGGGCCCTCTGAAGACAAAGAAACATG 1160
Qy 1191 TCAGCTTGTCTGGCAGGATGGCGGTCTTTTCGGGAAATGAACGTGGGTGGTGGACAGC 1250
Db 1161 TCGGCTGTGTGCAAGGAGGACGATCTTTCAGAAACAGAACCTGGGTGTGGATAGT 1220
Qy 1251 TGCACCAAGTGTACCTGCAAGAAATTTAAACCAATTTGCCACCAATCACTGCGCGCT 1310
Db 1221 TGTACCACTCTCACCTGCAAGAAATTTAAACAGTGTGCAATCAATCACTGCTCACT 1280
Qy 1311 GCAACCTGCGCCAGTTCACCTTTGTGGAAGGGAATGCTGCCCTTCTGCTCCACATCG 1370
Db 1281 GCAACTGTGTGCAACCCCACTTTTGTGGAAGGAGTGTCTTCCATCTCTGTTCACCTCT 1340
Qy 1371 GTGACGCTGAGGAGGCTGTCTCCGTGGCAGAGTGGACCCAGTGTCTGCTGACGCTGT 1430
Db 1341 CGAGACAACGATGAGGCTGTCTCCGTGGCAGAGTGGACCCAGTGTCTGCTCACTGT 1400
Qy 1431 GGCTCTGGGACCCAGCAGAGAGCGGCTCTGTGACGCTTCACCAAGCAACACCTGTTGGG 1490
Db 1401 GGCTCTGGGACCCAGCAGAGAGCGGCTCTGTGATGTCTACCAAGCAACACCTGCTGGC 1460
Qy 1491 CCCTCGATCCAGACACGCGCTTGCAGCTGAGCAAGTGTGACACCGGATCCCGGAGAC 1550
Db 1461 CCCTCCATTCAGACAAGACATGCAGTTTGGGCAATATGATAGGAAATCCGTGAGAAAT 1520
Qy 1551 GCGCGCTGAGCCACTGTCTACCTTGTCTCATGCTGTGACCTGTGGAGTGGCAAT 1610
Db 1521 GGAGCTGGAGTCACTGTGTACCTGTGTCTGCTCCGTGGTGTGGAGTGGCAAT 1580
Qy 1611 ATCACAGCATCCGTCTCTGCAACTCCCACTGCCAGTGGCCAGATGGGGCAAGAAATGCAAA 1670
Db 1581 GTCACCCGCATACGCTCTGCAACTCACCACTGCGCCCAATGGGTGGCAAGAACTGCAAG 1640
Qy 1671 GGGAGTGGCGGGAGACAAAGCCTGCCAGGGCGCCCATGCCCAATCGATGGCGCTGG 1730
Db 1641 GGCAGTGGCGGGAAACAAAGCCCTGCCAGCGTGTCTCATGCCCAATTTGATGGCGCTGG 1700
Qy 1731 AGCCCTGCTGCTGGTGTGGCTGTGCACTGTCACTGTGCTGCGGTGGGATCCGGAGCGC 1790
Db 1701 AGCCCTGCTGCTGGTGTGGCTGTGCAAGTTCCTGTGCTGGAGGATCCGTGAGGCG 1760
Qy 1791 ACCCGGCTGTCAACAGCCCTGAGCCTCAGTACGAGGAGGAAGGCTGCGTGGGGATGTG 1850
Db 1761 ACAGTGTGTTGCAACAGCCCTGAGCCCAAGTATGAGGGAAGGATGTGTCTGGGGATGTG 1820
Qy 1851 CAGAGCGTCAAGTGTGCAACAAAGAGAGCTGCCCGTGGATGGCTGTATTCACAAACCCC 1910
Db 1821 ACAGAAACACCAAAATGTGCAACAAAGAGAGCTGCCCTATTGATGATGCTATCCAAACCCG 1880
Qy 1911 TGTCTCCGGGAGCCAGTGTGAGAGCTTCCCGATGGTCCCTGTGATGCGGCTTCTGC 1970
Db 1881 TGTCTCCGTGGAGCAAGTGTGCAACAGCTTCCCGATGGCTCCTGGTCTGTGGTTCCTGC 1940
Qy 1971 CCTGTGGGCTTCTTGGGCAATGGCAACCCACTGTGTGAGGACCTGGAGAGTGTGCCCTGGTC 2030
Db 1941 CCAGTGGGCTTCTTGGGCAATGGCAACCCACTGTGTGAGGACCTGGATGATGTGCTGTGGTC 2000

Qy 2031 CCCGACATCTCTCTCCACCAGCAAGTGTCTCGCTGTGTCAACACTCACGCTGGCTTC 2090
Db 2001 CGAGATATCTCTCTCAATTAACAAAGCTTCCGCTGTGTCAACACCAACCCCTGGCTTC 2060
Qy 2091 CACTGCGCTGCGCTCCCGCCGATACAGAGAGACAGCCGCTGGGTGGCTGGA 2150
Db 2061 CACTGCGCTGCGCTTGTCCGCCACGCTACAAAGGGACCCACCTTCGGGATTTGGCTGGAG 2120
Qy 2151 CGAGCAAGAGCGGAAAGCAAGTGTGTGAGCCGCAAAACCCATGCAAGGACAAGACACAC 2210
Db 2121 GATGCTAAACAGAAAACAAAGTATGTGAGCGAGAGATCCGTGCAAGGACAAGACTCAC 2180
Qy 2211 AACTGCCACAAGACGCGGAGTGTACCTACCTGGGTCTACTTCAGGAGCCCATGTACAAAG 2270
Db 2181 AACTGCCACAAGACTGACAGAGTGTACCTACCTGGGCCACTTTCAGTGACCCCATGTACAAG 2240
Qy 2271 TGGCAGTSCCAGACAGGCTACGCGGCGACGGGTCTATCTCGGGGAGGACTCGGACCTG 2330
Db 2241 TGGCAGTSCCAGACTGGCTATGCAAGTGTGGGTCTATCTCGGGGAGGACTCAGACCTG 2300
Qy 2331 GACGGCTGGCCCAACCTCAATCTGTCTGCGCCACCAACGACCCACTACACTGCATCAAG 2390
Db 2301 GACGGTTGGCCCAACAGCAACCTGTGTGTCTACCAATGCCACTACACTGCGTCAAG 2360
Qy 2391 GATTAACGCCCCCATCTGCCAAATTTCTGGCAGGAGAACTTTTGACAAGAGCGGATTTGGC 2450
Db 2361 GACAACCTGCCCAACCTGCCAAATTTCTGGCAGGAGGATTTTGTAAAGAGCGGAATCGGA 2420
Qy 2451 GATGCTGTGATGATGACGATGACAATGACGTGTGACCGGATGAGAAGGACAACCTGCCAG 2510
Db 2421 GATGCTGCGAGAGGAGGATGATAACGACGGGTGAGCGATGAGAAGGACAATTTGCCCA 2480
Qy 2511 CTCTCTTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGTTGGGACCGCTGTGAC 2570
Db 2481 CTCTCTTTCAATCCCGCCAAATTTAGACTATGATAGGATGAGTTGGAGACCGCTGTGAC 2540
Qy 2571 AACTGCGCTTACGTGCAACACCTGCCAGATCGACACAGACACAATTTGGAGAGGATGAC 2630
Db 2541 AATTGCGCTTATGTGCAACAACCAAGCAGACAGATCGACACGGACAACAACCGTGAAGGGAC 2600
Qy 2631 GCCTGCTCCGTGGACATTGATGGGGACGATGCTCTCAATGACGAGACAATTTGCCCTAC 2690
Db 2601 GCCTGCTCTGTGGATATCGACGGGGATGATTTTCAATGAGCGAGACAATTTGCCGCTAT 2660
Qy 2691 GTCACAACTGACGAGAGGACACCGGATGCTGACGCTGTGGGGATCACTGTGACAAC 2750
Db 2661 GTCACAACTGACGAGAGACACACGCTGACGCGTTGGGACCACTGTGACAAC 2720
Qy 2751 TGGCCCTGTGTGCAACACCTTGACAGACCGAGCTGGACAATGACCTTTGTTGGGACCAAG 2810
Db 2721 TGTCTCTGTGATGCAATAACCCAGATCGATGGATCAGGACAATGATCTGTTGGAGACCAAG 2780
Qy 2811 TGTGACAACAAGAGGACATAGATGACGACGCCCAACAGACAACCAAGGACAACCTGCCCC 2870
Db 2781 TGTGATACATGAGGACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2840
Qy 2871 TACATCTCAACGCCAACAGGCTGACCATGACAGAGAGCGGACGAGCGGAGCGCTGTGAC 2930
Db 2841 TACATCTCAACTCCAACCGCTGACCATGACATGACATGACGCAAGGAGGATGCTGTGAC 2900
Qy 2931 CTTGATGATGACAGGATGGCGTCCCGATGACAGGAGACAATGCGCGCTGTGTCAAC 2990
Db 2901 TCCGATGATGACAAGTGTGTTCCAGATGACAGGAGACAATGCGAGGCTGTGTTCAC 2960
Qy 2991 CCAGACAGGAGGACTTGGACGCTGATGAGGCGGTGATTTTGTAAAGATGATTTTTCAC 3050
Db 2961 CCCGACCAAGAAAGCTCGGATGGCGACGGCCGAGGTGATTTTGTAAAGATGACTTTGAC 3020
Qy 3051 AATGACAACATCCCGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3110
Db 3021 ANTGATATGTTCCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3080

Db 205 CAGGTGGAGACAAGATGCTCTGGGCACTGGCCCTGGCTCTGGGCATAGGGCCAAAGAG 264
QY 286 CGCAAGCTGGTCCACGAGACAAACACAGCAGCCTTCGACCTTTTCAGTATCAAGCAACATCA 345
Db 265 CTTCTGCTGGTGACCAAGCTCAAGACACACTCAATTTGACCTTTTCAGATCAAGCAACATTA 324
QY 346 ACCCAAGAACCATTTGGGCGCCAAAGCAGTTCCGCGGCGCCGACCCCGGGGTGCCGGCTTACC 405
Db 325 ACCGGAAGACCATCGGTGCCAAGCAGTTCCGAGGGCCCTGACCCCGGGGTGCCGCCCTTACC 384
QY 406 GCTTTCGTGGCTTTGACTACATCCCAACCGGTGAACGGAGATGACCTCAGCAAGATCAACCA 465
Db 385 GTTTTGTACGCTTTGACTACATCCCGCCAGTGAACACAGATGATCTCAACAGGATTGTCA 444
QY 466 AGATCATGCGGCACAAAGAGGGCTTCCTTCACGCGGCCAGCTCAAGCAGGACCGCAAGT 525
Db 445 AGCTTGAAGAGAAAGAGGGCTTCCTTCACAGCCCACTGAAGCAGGACCGCCAGT 504
QY 526 CCAGGGGCACGCTCTGTGGCTCTGAGGGCCCGGCTCTCCACAGCAGCAGTTCCAGATCG 585
Db 505 CTCGGGAACGCTCCTGGTGTGGAAGCCCGCCGACCTCCACAGGCGAGTTTGAGATTG 564
QY 586 TCTCCAAAGCCCGCGGACACGCTGGATGATCTACCTACTGGAATGACGGCACCGCGCATG 645
Db 565 TGTCCAATGGCCAGGGGACACTTTGGACCTCAACTACTGGGTAGAGGCAATCAGCAT 624
QY 646 TGGTCTCCCTGGAGAGCTGGCCCTGGCTGACTCGAGTGAAGAAAGCTCAACCTGCAAG 705
Db 625 CCAATCTCTGGAGGATGTGGGCTGGCTGACTCCCAAGTGAAGAAATGACTGTGCAAG 684
QY 706 TGGCTGGGAGACCTACAGCTTGACGCTGGGCTGGGCTCGACCTCATAGGACCAAGTCTCTGG 765
Db 685 TGGCCAGTGACACCTATAGCCCTGTATGGGCTCGGACTTATCGACAGTGTCAACCTGG 744
QY 766 ACGAGCCCTTCTACGAGCACCTCGAGCGGAAAGACCGGATAGCTGGCCAAAGGCT 825
Db 745 AAGAACCATCTATAGCAGCTAGAAGTAGACAGGACGAGATGACTGCGCAAGAGTG 804
QY 826 CTGCCAGAGAGTCACTTCAGGGGTTTGTTCAGAGCTGCCACTAGTGTTCGAAACT 885
Db 805 CATCTCAGAGAGTCACTTCAGGGGCTTGTGCAAGATGTCCATCTCGTGTTCAGATT 864
QY 886 CTGTGGAAGATATTCTAAGCAAGAGGTTGCCAGCAGGCGAGGAGCTGAGATCAAGC 945
Db 865 CTGTGGAAGATATTCTAAGCAAGAAAGCTGTCAACACAGCCAGGAGCTGAAGTCAACA 924
QY 946 CCATCAGTGAACATACAGAGACTCTCCATCTGAGCCCTCAGTCAACACAGATCTCGTGG 1005
Db 925 GCTTGGAGATATTCTAAGCAAGAAAGCTGTCAACACAGCCAGGAGCTGAAGTCAACA 924
QY 1006 GCTTGGAGATATTCTAAGCAAGAAAGCTGTCAACACAGCCAGGAGCTGAAGTCAACA 1065
Db 985 TCCAGGCTGTGGAGAGGCAAGAGGTTGTACGCATCTCTGCGAGGAGTTGAGCAACA 1044
QY 1066 TGTTCAGGAGCTCTCGGGGCTCACCTCTCTGTAACACAGCTCAGCAGAGAACCTCAAGA 1125
Db 1045 TGATGATGAGCTCTGTGGAGTGCACGTGATGGTGAACAGCTGAGCAAGAACCTTGAGA 1104
QY 1126 GAGTGTGGAATGATAACAGTTTCTCTGGAGCTCATTTGTTGGCCCTCTCTAAGCAAGGA 1185
Db 1105 GAGTGTGATGATAACAGTTTCTCTGGAGCTCATTTGTTGGGCGCTCTGAGACAGAA 1164
QY 1186 ACATGTAGCTGTGGAGATGAGGCGGTTCTTGTGGGAAATGAAACGTTGGTGGTGG 1245
Db 1165 ACATGTAGCTGTGGAGATGAGGCGGTTCTTGTGGGAAATGAAACGTTGGTGGTGG 1224
QY 1246 ACAGTGCACACCTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATCACCTGCC 1305
Db 1225 ATAGTTGACACATGACCTGTCAAGAAATTTAAACAGCTGTGCCATCAGATCACCTGCT 1284
QY 1306 CGCTGCAACCTGCGCAGTCCATCTTGTGGAGGCAATGCTGCGCTTCTCTGCGCTCC 1365
Db 1285 CACCTGCAACTGTGCAACCCATCTTTGTGGAAAGGAGTGTCTCCATCTCTGTTTCA 1344

QY 1366 ACTCGTGGACGGTGGAGAGGGCTGGTCTCCGTGGGCAAGAGTGGACCCAGTGTCTCCGTGA 1425
Db 1345 ACTCTGAGACAGTGGATGAGGGCTGGTCTCCGTGGGCAAGAGTGGACCCAGTGTCTCTGTC 1404
QY 1426 CGTGTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGAGCTCACCAGCAACACCTGCT 1485
Db 1405 CCTGTGGCTCTGGGACCCAGCAGAGAGGCGGCTCTGTGATGTCCACAGCAACACCTGCC 1464
QY 1486 TGGGGCCCTCGATCCAGACAGGCGCTTGCAGTCTGAGCAAGTGTGACACCCGCAATCCGGC 1545
Db 1465 TGGGCCCTCCATTCCAGACAGGACATGACGCTGGGCAAAATGTGATACAGAAATCCGTC 1524
QY 1546 AGGACGGGCTGGAGCCACTGGTCACTTGGTCTTCATGCTCTGTGACCTGTGAGTTG 1605
Db 1525 AGAATGAGGCTGGAGTCACTGGTCACTGGTCTTATGCTCCGTGACTTGTGGAGTTG 1584
QY 1606 GCAATATCACACGATCCGCTCTGCAACTCCCAAGTGGCCAGATGGGGGCAAGAAAT 1665
Db 1585 GCAATGTACCCCGCATAGCTCTGCAACTCCCAAGTGGCCAGATGGGGGCAAGAAAT 1644
QY 1666 GCAAAGGAGTGGCCGGAGACCAAGCCCTGCCAGGCGGCCCATGCCAATCGATGGCC 1725
Db 1645 GCAAGGCGAGGCGCGGAAACCAACCCCTGTGACGCTGTATCCGTCGCCAATTTGATGCC 1704
QY 1726 GCTGGAGCCCTGTGCTCCCGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1785
Db 1705 GCTGGAGCCCTGTGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1764
QY 1786 AGCCACCCCGGCTGCAACAGCCCTGAGCCTGAGTGGAGGAGGAGGAGGAGGAGGAGG 1845
Db 1765 AGCCCTCAGCTGTGTGCAACAGCCCTGAGCCCGAGTGGAGGAGGAGGAGGAGGAGG 1824
QY 1846 ATGTGAGGAGCGCTCAGATGTGCAACAGAGAGCTGCCCGTGGATGGCTGTATATCCA 1905
Db 1825 ATGTGAGAGAACACCAATGTGCAACAGAGAGAGTGGCTGTATGATGGGTCATATCCA 1884
QY 1906 ACCCTGTTCCCGGAGCCAGTGGAGAGCTTCCCGATGGGTCTGCTGCTGCTGCTGCTGCT 1965
Db 1885 ACCCTGTTTCTTGGAGCAAGTGGCAACAGCTTCCCTGATGGTCTGCTGCTGCTGCTGCT 1944
QY 1966 TCTCCCTGTGGGCTTCTTGGGCAATGGCACCCTGAGGAGCTGGACGAGTGGCC 2025
Db 1945 CTGCCCAGTGGGCTTCTGGGCAATGGTACCCTGAGGAGCTGGATGAGTGGTGGTGG 2004
QY 2026 TGTTCCTCCGACATCTGCTTCTCCACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2085
Db 2005 TGTTCACAGATATTTGCTTCTCAACTAACAAAGCTCCCGCTGTGTCAACACCAACCCGG 2064
QY 2086 GCTTCCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2145
Db 2065 GCTTCCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2124
QY 2146 TGGAGCAGCCCAAGCAGGAAAGCAAGTGTGTGAGCCCGGAAACCCATGCAAGGACAGA 2205
Db 2125 TGGAGGATGTAGGACAGAAACAGTGTGTGAGCCAGAGAAATCCATGTAAAGGACAGA 2184
QY 2206 CACACAACTGCAACAGCAGCGGAGTGCATCTACCTGGGTCACTTTCAGCCAGCCCATGT 2265
Db 2185 CTCACAGTGCACAGAAATGACAGTGCATCTACCTGGGCCACTTTAGTACGCCCATGT 2244
QY 2266 ACAAGTGGAGTGCACAGAGCTTACGGGCGAGCGGCTCATCTGCGGGGAGGAGTGG 2325
Db 2245 ACAAGTGTAGTGCAGATTGGCTTACGAGGCTGATGGGCTCATCTGCGGGGAGGAGTCCAG 2304
QY 2326 ACCTGGAGGCTGGCCCACTCAATCTGCTGCGCCAGCAACCCAGCCCTACCTACCTGCA 2385
Db 2305 ACCTGGATGGTGGCCCACTGCAAAATCTGGGCAAGAACTTTGACAAAGCAGGGA 2445
QY 2386 TCAAGGATAACTGCCCCCATCTGCAAAATCTGGGCAAGAACTTTGACAAAGCAGGGA 2424
Db 2365 TCAAGGACACTGCCCCCACTGCCAAATTCGCGGAGGAGGATTTTGTATTAAGGATGGA 2424

Db 745 AAGAACCACTTCTATGACGACCTGACAGCTAGACAGGACGAGATGTACCTGCCCCAAGGTG 804
Qy 826 CTGCCAGAGAGAGTCACTTTCAGGGGTTTGCTTCAGAACGTCACCTAGTGTGTTGAAAAC 885
Db 805 CATCTCGAGAGAGTCACTTTCAGGGGTTTGCTTCAGAACGTCACCTAGTGTGTTGAAAAC 864
Qy 886 CTGTGGAGATATCTTAAGCAAGAGGTTCCAGAGAGGTCACGAGGACGAGCTGAGATCAACG 945
Db 865 CTGTGGAGATATCTTAAGCAAGAGGTTCCAGAGAGGTCACGAGGACGAGCTGAGATCAACG 924
Qy 946 CCATCAGTGAGAACACAGACGCTGCGGCTGGTTCGCGATGTCCACACCGAGTACGTGG 1005
Db 925 CCATCAGTGAGAACACAGACGCTGCGGCTGGTTCGCGATGTCCACACCGAGTACGTGG 984
Qy 1006 GCCCAGCTCGGAGGAGGCGGAGGTGCGGAGCGCTCGTGGAGAGTGGGAAACA 1065
Db 985 TCCAGGGTGTGGAGAGGACAGAGGTTGTACGACCTCTCGTGGAGGAGTTGAGCAACA 1044
Qy 1066 TGGTCCAGGAGCTCTCGGGGCTCCACCTCCCTGCTGACACGCTCAGCGAGAACCTCAAGA 1125
Db 1045 TGATGATGAGCTCTGTGGAGTGCACGTATGTTGTAACCGAGCTGAGCAAGAACCTGGAGA 1104
Qy 1126 GAGTGTGGAATGATTAACAGTTTCTCTGGAGCTCATTTGTTGGCCCTCCCTAAGACAAAGGA 1185
Db 1105 GAGTGTGATGATAACAGTTTCTCTGGAGCTCATTTGTTGGCCCTCCCTGGAAGACAAAG 1164
Qy 1186 ACATGTGAGCTGTGCGAGAGTGGCGGTTCTTTCGGGAAATGAAACGTTGGTGTGG 1245
Db 1165 ACATGTGAGCTGTGCGAGAGGCGGAAATTTTTCGAGAAATGAAACCTGGGTTGTGG 1224
Qy 1246 ACAGCTGCACACGCTGTACCTGCAAGAAATTTAAACCATTTGCCACCAATCACCTGCC 1305
Db 1225 ATAGTGTACCAATGACCTTGCAGAAATTTAAACAGCTGTCATCAGATCACCTGCT 1284
Qy 1306 CGCTGCAACCTGCGCAGTCCATCTCTTGTGGAAGCGAATGTCCTTCCTGCGCTCC 1365
Db 1285 CACCTGCAACTTGTGCCAACCCATCTTTTGTGGAAGCGAGTGTCTCCATCTCTTCAC 1344
Qy 1366 ACTCGTGGAGGTTGAGAGGCTGTGCTCGTGGGAGAGTGTGACCCAGTGTCCGTTGA 1425
Db 1345 ACTCTGAGACAGTGTGATGAGGCTGTGCTCGTGGGAGAGTGTGACCGAGTGTCTGCA 1404
Qy 1426 CGTGTGCTCTGGACACGAGAGGCGGCTCTGTGAGCTCACCAGCAACACCTGCT 1485
Db 1405 CTTGTGCTCTGGAGCCAGCAGAGAGGCGGCTCTGTGATGTACCAGCAACACCTGCC 1464
Qy 1486 TGGGGCCCTCGATCCAGACAGGCTTGCAGTCTGAGCAAGTGTGACCCCGCATCCGGC 1545
Db 1465 TGGGCCCTCCATTCAGACAAAGACATGCAGCTTGGGCAAAATGTATACGAGATCCGTC 1524
Qy 1546 AGGAGCGGCTGAGCCACTGTGCTACCTTGGTCTTATGCTCTGTGACCTGTGGAGTTG 1605
Db 1525 AGAATGAGGCTGAGTCACTGTGTCACCTGCTTCTATGCTCTGCTGCTGCTGCTGCTG 1584
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Db 1585 GCAATGTACCCCGATAGTCTCTGCAACTCACAGTGCACCGATGGTGGGCAAGAACT 1644
Qy 1666 GCAAGGAGTGGCGGAGACCAAAAGCCTGCGAGGCGCCCATGCCCCAATCGATGCC 1725
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Qy 1726 GCTGGAGCCCTGTGCTCCGCTGTGCTGCGCTGCACTGTACCTGTGCGGCTGGAGTCCGG 1785
Db 1705 GCTGGAGCCCTGTGCTCCGCTGTGCTGCACTGTACAGTGTACCTGTGCTGAGGAGTCCGTG 1764
Qy 1786 AGCCACCCCGGCTGCAACAGCCCTGAGCTCAGTACGAGGAGGAGGAGGAGGAGGAGG 1845
Db 1765 AGCCCTACGTTGTGCAACAGCCCTGAGCCCGAGTATGAGGAGGAGGAGTGTGCTCGGG 1824
Qy 1846 ATGTGAGGAGGCTGAGATGTGCAACAGAGGAGCTGCCCGCTGGATGGCTGTTATCCA 1905
Db 1825 ATGTGAGAGAACACCAAAATGTGCAACAGAGAGAGCTGCCCTATGTGATGGGTGCTTATCCA 1884

Qy 1906 ACCCTGCTTCCCGGAGCCAGTGCAGCAGCTTTCOCGATGGGTCTGTGCTATGCGGCT 1965
Db 1885 ACCGCTGTTTCCCTGGAGCCAAAGTGCACACAGCTTCCCTGATGGGTCTGTGCTGTGCT 1944
Qy 1966 TCTGCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGACAGTGTGCC 2025
Db 1945 CTTGCCAGTGGGCTTCTTGGGCAATGGTACCCACTGTGAGGACCTGGATGAGTGTGCTG 2004
Qy 2026 TGTTCCTCCGACATCTGCTTCTCCACCAAGAGTGCCTTCGCTGTGTCAACACTCAGCCTG 2085
Db 2005 TGTTCACAGATATTTGCTTCTCACTAACAAAGCTCCCGCTGTGTCAACACCAACCGG 2064
Qy 2086 GTTTCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2145
Db 2065 GTTTCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2124
Qy 2146 TGGAGCAGCCACAGCAAGAAAGTGTGTGAGCCCGGAAACCCATGCAAGACACAGA 2205
Db 2125 TGGAGGATGTGAGCAGAAACAAAGTGTGTGAGCCAGAGATCCATGTAAGGACAGA 2184
Qy 2206 CACAACTGCAACAGCAGCGGAGTGCATCTACCTGGGTCACTTCAGCGACCCCATGT 2265
Db 2185 CTCACAGCTGCCACAAGATGTCAGAGTGCATCTACCTGGGCACTTTAGTCAACCCATGT 2244
Qy 2266 ACAAGTGGAGTGCAGACAGGCTTACGCGGCGCAGCGGCTCATCTGCGGGGAGGACTGG 2325
Db 2245 ACAAGTGTGAGTGCAGATTTGGCTTACGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2304
Qy 2326 ACCTGGAGGCTGCGCCAACTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2385
Db 2305 ACCTGGAGTGTGCGCCCAACAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2364
Qy 2386 TCAAGGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2445
Db 2365 TCAAGGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2424
Qy 2446 TTGCGGATGCTGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2505
Db 2425 TCGGAGATGCTTGTGAGGAGGACGATGACATGACGCTGTGAGCGATGAGAGGACAAAT 2484
Qy 2506 GCCAGCTCTCTTCAATCCCGCAGGCTGACTATGACAGGATGAGGTGCGGACCGCT 2565
Db 2485 GCCAGCTCTCTTCAATCCCGCAGGCTGACTATGACAGGATGAGGTGCGGACCGCT 2544
Qy 2566 GTGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2625
Db 2545 GTGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2604
Qy 2626 GTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2685
Db 2605 GGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2664
Qy 2686 CTAAGTCTTCAACACTGACCAAGGACACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2745
Db 2665 CATATGCTTCAACACTGACCAAGGACACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2724
Qy 2746 ACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2805
Db 2725 ACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2784
Qy 2806 ACCAGTGTGACAAACAGGAGACATAGATGACGAGCGGCGCCACCAACCA 2857
Db 2785 ACCAGTGTGACAAACAGGAGACATAGATGACGAGCGGCGCCACCAACCA 2836

RESULT 12

AAZ32052

ID AAZ32052 standard; DNA; 5289 BP.

XX

AAZ32052;

XX

DT 10-JAN-2000 (first entry)

XX Human METH2 related EST AB005287.
 XX DE
 XX Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;
 KW arterial-venous malformation; immune deficiency; ss.
 XX OS
 XX Homo sapiens.
 XX WO937660-A1.
 XX PN
 XX 29-JUL-1999.
 XX PD
 XX 22-JAN-1999; 99WO-US01313.
 XX PF
 XX 23-JAN-1998; 98US-0072298.
 XX PR
 XX 28-AUG-1998; 98US-0098539.
 XX PR
 XX (IRUE/) IRUELA-ARISPE L.
 XX PA (HAST/) HASTINGS G A.
 XX PA (RUBE/) RUBEN S M.
 XX PI
 XX IrueLA-Arispe L, Hastings GA, Ruben SM;
 XX WPI; 1999-590684/50.
 XX DR
 XX New isolated metalloprotease thrombospondin polypeptides, useful for
 XX PT treating hyperproliferative disorders, cancers or autoimmune disorders
 XX PT
 XX Disclosure; Page 414-418; 457pp; English.
 XX PS
 XX AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human
 XX CC metalloprotease thrombospondin (METH) proteins METH1 and METH2
 XX CC respectively. METH1 and METH2 have been found to be potent inhibitors of
 XX CC angiogenesis both in vitro and in vivo. They can be used for treating
 XX CC cancer and other disorders related to angiogenesis including abnormal
 XX CC wound healing, inflammation, rheumatoid arthritis, psoriasis,
 XX CC endometrial bleeding disorders, diabetic retinopathy, some forms of
 XX CC macula degeneration, haemangiomas, and arterial-venous malformations.
 XX CC They may be useful in treating deficiencies or disorders of the immune
 XX CC system, by activating or inhibiting the proliferation, differentiation,
 XX CC or mobilisation (chemotaxis) of immune cells. The etiology of these
 XX CC immune deficiencies or disorders may be genetic, somatic, such as
 XX CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
 XX CC toxins), or infectious. They can also be used to treat inflammatory
 XX CC conditions, both chronic and acute conditions. The products can also be
 XX CC used for detection and diagnosis. AA232002 to AA232080, and AAY49503 to
 XX CC AAY49511 represent sequences given in the exemplification of the present
 XX CC invention.
 XX SX
 XX Sequence 5289 BP; 1380 A; 1378 C; 1366 G; 1165 T; 0 other;
 XX
 Query Match 27.7%; Score 1604.2; DB 20; Length 5289;
 Best Local Similarity 66.1%; Pred. No. 0;
 Matches 2392; Conservative 0; Mismatches 1193; Indels 32; Gaps 4;
 QY 152 CTGCGCCTTTCTGACTCGTCCGGAACACTGAAACAGTCATCATCTGCTCTTTGGCA 211
 DB 72 CTGCGCCTTTGTCGCGCGCGCGCGCTGTCATCGCGTCCGCAACAGGCTCTCTGCTGG 131
 QY 212 AACCAAGAGCTCAGCTGAGGAGGAGGAGTGTCTGGAGGCTGGTCTGCTGCTGCTGTG 271
 DB 132 CACAAATAGCTCCACCATGGGCTGGCTGGGACTCGGTGTCTGCTGCTGCTGCTGCTG 191
 QY 272 GGTGTGGCCACGACGAGTGTGTACCAAGGACAAAGACAGACGCTTTCGACCTTTTCAG 331
 DB 192 CTGCGGCTCCAAACCGCATTTCCAGAGTCTGGGGGAGACAAACAGTGTGTTGACATCTTGA 251
 QY 332 TATCAGCAACATCAACCGCAAGACCATTTGGCGCCCAAGCAGTTCGCGGGCGCCCGCGG 391

DB 252 ACTCAGCGAGCTGCGCGCAAGCGGTCTGGGCGCCGACTGGTGAAGGGCCCTGACCTTC 311
 QY 392 CGTCCGCGCTTACCGCTTCTGCTGGCTTTGACTACATACCTCCACCGGTGAACGACAGTACCT 451
 DB 312 TAGCCAGCTTTCCGATCGAGATGCCAACTGATCCCGCTGTGCTGCTGCTGCTGCTGCTGCT 371
 QY 452 CAGCAAGATACCAAGATCATCGCGCAGAGGAGGCTTTCTTCTCCTCAGCGCCAGCTCAA 511
 DB 372 CCAAGACCTAGTGGATGCTGCGGGCGGAGAAAGTTTCTCTCTCTCTCTCTCTCTCTCTGAG 431
 QY 512 GCAGNACGCAAGTTCAGGGGACGCTGTTGGCTCTGAGGGGCGCGGCTTCTTCCAGAG 571
 DB 432 GCAAAATGAAGAACCGCGGGTACCTGCTGGCTGTGGAGCGGAAGACCACTCTGGCCA 491
 QY 572 GCAGTTCGAGATCGTCTCAACGCGCGCGACACGCTGCGATCTCACTACTGGATTGA 631
 DB 492 GGTCTTCAGCTGATCTCCAAATGGCAAGCGGGCACCTTGGACCTGAGCCTGACCGTGA 551
 QY 632 CGGCACCGGCTGCTGCTCCCTGGAGACGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
 DB 552 GGGGAAGCAGCATGTGCTGCTGGTGAAGAACCACTCTCTGGGCTGCTGCTGCTGCTGCTGCTG 611
 QY 692 CGTACCGTGCAGTGGCTGGCGAGACCTACAGCTTGCAGTGGGCTGGGCTGCTGCTGCTGCTGCT 751
 DB 612 CATCACCTGTTGTGTCAGAGGACAGCGGCCACAGCTGTACATCGACTGTGAGAGATGA 671
 QY 752 ACCAGTGTCTCTGACGAGCGCTTCTAGCAGCACTTGCAGGCGGAAAGAGCGGATGA 811
 DB 672 GAATCGGAGCTGGATGCTCCCATCCA -GAGCATCTTCCAGGAGCTGCTGCGACATGG 730
 QY 812 CGTGCCAAAGGCTCTGCGCAGAGAGAGTCACTC-----TTCAGGGGTTTGTCTCAGAACG 864
 DB 731 CCAGGCTCGCATTTCCAAAGGAGGTGTCAAGACAAATTTCCAGGGGTTGCTGCGAATG 790
 QY 865 TCCACTAGTGTTCGAAACTCTGTGGAGATATTTCTAAGCAAGAGGTTGCCAGCAAG 924
 DB 791 TAAGTGTGCTTTTGGAACTCACCAAGAGACATCTCTCAGGAACAAGGCTGC-----T 844
 QY 925 GCAGGGAGCTGAGATCAACGCCATCAGTGAACACAGAGACGCTGCGCTGGTCCGCGC 984
 DB 845 CCAGCTCTACAGTGTCTTTGTACACCTTGACAAACAGTGTGTAAGTGGTCCAGCCCTG 904
 QY 985 ATGTCCACCGAGTACGTGGGCGCCAGCTCGGAGAGGAGGCGCGAGGTGTGCGAACGCT 1044
 DB 905 CCATCCGACCGACTACATTTGGCCCAAGAACAAAGAGCTGCAAGCCATCTGTGCGCATCT 964
 QY 1045 CGTGCGAGAGCTGGGAACATGTTCTCAGGAGCTCTCGGGGCTCCAGCTCTCTCTGCTGTAACC 1104
 DB 965 CATGTGACGAGCTGTCCAGCATGGTCTTGGAGCTCAGGGGCTTACGCCACCATCTGTAACA 1024
 QY 1105 AGCTCAGCGAGAACCTCAAGAGAGTGTGCAATGATAACAGTCTCTCTGGAGCTCATTTG 1164
 DB 1025 CGCTCAGCAGCATATCCGAAAGTGACCGAGAGAACAAAGAGCTGGCCACAGAGCTGA 1084
 QY 1165 GTGGCCCTCTTAAGACAAAGAACATGTGCTGCTGAGAGTGGCGGTTCTTTGGGG 1224
 DB 1085 GGAGGCCCT-----CACCTGTCTACCAACAGGAGTGCAGTACAGCA 1126
 QY 1225 AAATGAACGTTGGTGTGTGACAGCTGCACCACTGTACCTGCAAGAAATTTAAACCA 1284
 DB 1127 CTGGCAGAGTGGAGGCTGGAGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1186
 QY 1285 TTTGCGACAAATACCTTGGCGCGCTGCAACTGGCGCAGTCCATCTTGTGGAAGCG 1344
 DB 1187 TCTGCAAAAGTGTCTGTCCCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246
 QY 1345 AATGCTGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
 DB 1247 AATGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1306
 QY 1405 AGTGACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464

Db 1307 AGTGGACCTCTTGTCTGTGACCTGTGGCAATGGAAATCCAGCAGCGTGGCGCTCCTCGG 1366
Qy 1465 ACGTCAACCAAGACACCTGCTTGGGGCCCTCGATCCAGACACGGGCTTGAGCTGTGAGCA 1524
Db 1367 ACAGCCTCAACACACAGATGTGAGGGCTCTCTGTGTGAGAGCGGACCTGCCACATCCAGG 1426
Qy 1525 AGTGTGACACCCGATCCGGCAGGACGGCGCTGAGCCACTGGTCACTTGGTGTCTTCAT 1584
Db 1427 AGTGTGACAGAGATTTAAACAGAGATGGCGCTGGAGCCACTGGTCCCATGGTCATCTT 1486
Qy 1585 GCTCTGTGACCTGTGGAGTGTGGCAATATACACGCACTCCGCTCTCTGCAACTCCCCAGTGC 1644
Db 1487 GCTCCGTAAATGTGGAGACGGTGTGATCACAAGGATCCGGCTCTGCAACTCCCCAGCC 1546
Qy 1645 CCCAGATGGGGGCAAGAAATGCAAGGAGTGGCCGGGAGACAAAGCCTGCCAGGGG 1704
Db 1547 CCCAGATGAATGGGAAGCCATGTGAGGGCAAGGCCGGGAGACAAAGCCTGCCAGAAAG 1606
Qy 1705 CCCCATGCCCAATCGATGGCGCTGGAGCCCTGCTGCCGTGGTGGCGCTGCACTGTCA 1764
Db 1607 ACTCCTGCCCATCAATGGAGCTGGGACCTTGGTCACCATGGGACATCTGTTCTGTCA 1686
Qy 1765 CTTGTGCGGTGGATCCGGGAGCGCACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACG 1824
Db 1667 CCTGTGGAGGAGGGGTACAGAAACGTAGCCGGCTCTGCAACAAACCCCAACCCCACTT 1726
Qy 1825 GAGGAAGGCTGGTGGGGATGTGAGGAGCGTCAAGTGTGCAACAGAGAGCTGCC 1884
Db 1727 GAGCAAGGACTGCGTTGGTGTGATGTGACAGAAACACAGATCTGCAACAGCAGGACTGC 1786
Qy 1885 CCGTGGATGGCTGTTTCAACCCCTGCTTCCGGGAGCCAGTGCAGCAGCTTCCCG 1944
Db 1787 CCATGAGGATGCTGTCNAATCCCTTGTGTGTGTCAGTACAGCTACCCCTG 1846
Qy 1945 ATGGGTCTGTATGCGGCTTCTGCCCTGTGGCTTCTTGGGCAATGGCACCCACTGTG 2004
Db 1847 ATGCACTGGAAGTGGTGGCTGTCCCGCAGGCTATAGTGGAGATGGATCGAGTGCA 1906
Qy 2005 AGGACCTGGAGCAGTGTGCCCTGTGCCCGACATCTGCTTCTCACCAAGCAGTGGCTG 2064
Db 1907 AAGAGCTGTGATGTGCAAGAGATCTCCTGATGCTCTTCAACCAATGGAGAGACA 1966
Qy 2065 GCTGTGCAACACATCAGCTGGCTTGAAGCAGCCAAAGCGGAAACAAAGTGTGTGAGCCG 2124
Db 1967 GGTGTGAGACACAGACCCGGCTACAACTGCTTGGCTGCCCTGCCACCGGCTTCACTGGCT 2026
Qy 2125 ACCAGCCGCTGGGGTCTGGCTGGAAGCAGCCAAAGCGGAAACAAAGTGTGTGAGCCG 2184
Db 2027 CGCAGCCCTTTGGCGGGCGTGGAACTGCCACCGCCCAACAGCAGTATGCAAGCCCC 2086
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Db 2087 GAAACCCCTGCACAGAGGGGACACAGCTGCAACAAAGAGCCCAAGTGTCAACTACCTGG 2146
Qy 2245 GTCACTTCAGGACCCCATGTACAAAGTGGAGTCCAGACAGGCTACGCGGCGCAGCGGC 2304
Db 2147 GCCACTACAGCGCCCATGTACCGCTGCGAGTGCAGCTGGCTACGCGGCAACGCA 2206
Qy 2305 TCATCTCGGGGAGGACTCGGACCTTGGACGCTGGCCGCTGCCCAACTCAATCTGTGTGCGGCA 2364
Db 2207 TCATCTCGGGGAGGACACAGACCTGACGCGCTGGCCCAATGAGGACCTGTGTGCGTGG 2266
Qy 2365 CCAAGGCCACTTACCATGTCAAGATNACTGCCCCCATCTGCCAAATCTCGGGGAGG 2424
Db 2267 CCAACGCAACTTACCATGTCAAGAAAGATATTTGCCCAACTTCCCAACTCAGGGGAGG 2326
Qy 2425 AAGACTTTGACAAGGAGGATTCGGCATGCGCTGTGTGATGATGAGATGACAAATCACGGTG 2484
Db 2327 AAGACTATGACAAGGATGGAATGGCGCATGCTCGGATGATGAGATGACAAATGATAAGA 2386
Qy 2485 TGACCGATGAGAAGGAACTTCCAGCTCTCTTCAATCCCGCCAGGCTGACTATGACA 2544
Db 2387 TTCAGATGACAGGACAACTGTCCATTCCATTACACCCAGCCAGCTACGACTATGACA 2446

Qy 2545 AGGATGAGGTTGGGACCGCTGTGCAAACTGCCCTTACGTGCAACAACCTGCCAGATCG 2604
Db 2447 GAGATGACGTGGGAGACCGCTGTGACAACTGCCCTTACAAACCAACCCAGCAGGCTG 2506
Qy 2605 ACACAGACAACAAATGTGAGAGGGTGACCGCTGCTCGTGGACATTTGATGGGGACCATGTCT 2664
Db 2507 ACACAGATAACAATGGGAGGAGACCGCTGTGAGCTGACATTTGATGGGGACAGTATCC 2566
Qy 2665 TCAATGAACAGAGACAATTTGTCCCTACGTCTACAACTGACACAGAGGACACCGATGGT 2724
Db 2567 TCAATGAACGGGACAACCTGCCAGTATGTCTACAATGTGGACCAAGAAAGACACTGACATGG 2626
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Db 2627 ACGGGGTGGTGTGATCAGTGTGACAACTGCCCTTGGAAACAACATCCAGACAGCTCGACT 2686
Qy 2785 TGGCAATGACCTTGTGGGACCACTGTGACAAACAGGAGACATAGATCACCACGGCC 2844
Db 2687 CTGACTCGGACCGCATTTGGAGACACCTGTGACAACTACAGATATTTGATGAACAGGCC 2746
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Db 2807 AGGATGGCAAGCGGATGGCTGTGACCATGATGACGAATGATGGCATCTCTGATGACC 2866
Qy 2965 GGGACAACCTGCCGCTTGTGTTCAACCCAGACAGGAGGACTTGCAGGTGATGACGCGG 3024
Db 2867 GGGACAACCTGAGCGCTGTGCCCAATCTGACCAAGAGGACTGTGATGGTGTGATGTCAG 2926
Qy 3025 GTGATATTTGTAAGATGATTTTGACAAATGACAACTCCCAAGATATTTGATGATGTGTGTC 3084
Db 2927 GTGATGTTGCAAAAGATGATTTTCCACAGGCAAGGTGCCAGACATGATGACATCTGTC 2986
Qy 3085 CTGAAACAATGCCATCAGTGAGACAGACTTCAGAACTTCCAGATGGTCCCTTTGGATC 3144
Db 2987 CCGAAAATGTGTATCAGTGAGACTGATTTCCGCCGATTTCCAGATGATTTCTCTAGATC 3046
Qy 3145 CCAAGGACCCCAAAATGATCCCAACTGGCTATTTCGCCCAATCCAGATGATTTCTCTAGATC 3204
Db 3047 CCAAGGACATCCAGATGACCCCTTACTGGGTGTACGCCATCAGGGTAAAGAACTCG 3106
Qy 3205 TTCAGACAGCAACTCGGACCCCGGCTGCTGTAGTGTGAGAGTGTGGGTCTGTGG 3264
Db 3107 TCCAGACTGTCAACTGTGACCTTGGACTTGTGTAGTGTATGACGAATTTAAACGCGTGG 3166
Qy 3265 ACTTCAGTGGCAATTTCTACGTAACACTGACCGGGACGAGCACTATGCTGGCTTGTCT 3324
Db 3167 ACTTCAGTGGCACTTCTTCATCAACACCGAGAGGATGAGCACTATGCCGGCTTGTGT 3226
Qy 3325 TTGTTTACCAGTCAAGCAGCGCTTCTATGTGTGTGATGTGAAGCAGGTGACGAGACT 3384
Db 3227 TTGCTTACCAGTCCAGACGCGCTTCTATGTGTGTGATGTGAAGCAAGTCACTCAGTCT 3286
Qy 3385 ACTGGGAGGACCAAGCCACGCGGCTTATGCTACTCTCCGGCTGTCCCTCAAGTGTGTA 3444
Db 3287 ACTGGACACCAACCCACAGGCTCAGGGGTACTCTGGACTTTCCTGGAAGTTGTAA 3346
Qy 3445 ACTCCACACGGGACGGCGGAGCACTGAGGAACGCGCTGTGGCACACGGGGAACAGCC 3504
Db 3347 ACTCCACACGGGCGCTGGCAGCACCCTGCGGAATGCCCTGTGGCACACAGGAAACACT 3406
Qy 3505 CGGGCAGGTGCGAACCTTATGGCAGCAGCCCAAGCAATTTGGTGTGAAGACTACAGG 3564
Db 3407 CTGGCAGGTGCGCACACTGTGGCATACCTCGCTCAGTACATTTGGCTGGAAGATTTCACTG 3466
Qy 3565 CCTATAGTGGCACTGACTCACAGGCGCAAGACGGGTACATCAGAGTCTTACTGTGATG 3624
Db 3467 CCTACAGATGGCACTGAGCCACAGGCCAAAGACAGGTTTTCATCAGAGTGTATGTATG 3526

QY 3625 AAGGAAACAGGTCATGGGAGACTCAGGACCTATCTATGACCAAAACCTACGCTGGCGGCGC 3684
 DB 3527 AAGGGAAGAAATCATGGCTGACTCAGGACCCATCTATGACAAAACCTATGCTGGTGGGA 3586
 QY 3685 GCGTGGTCTATTGCTCTCTCAAGAAATGCTCTATTCTCAGACCTCAAGTAGGAAT 3744
 DB 3587 GCGTAGGCTGTTGCTCTCTCAAGAAATGCTGCTCTCCGACCTGAAATATGAAT 3646
 QY 3745 GCAGAGATATTTAAACA 3761
 DB 3647 GCAGAGACTCCTAATCA 3663

RESULT 13
 AAC90309
 ID AAC90309 standard; DNA; 5289 BP.
 XX
 AC AAC90309;
 DT 19-MAR-2001 (first entry)
 XX
 DE AB005287 cDNA clone.
 XX
 KW METH; metalloproteinase; thrombospondin; angiogenesis inhibition;
 KW cancer therapy; benign tumour; ocular angiogenic disease;
 KW rheumatoid arthritis; psoriasis; wound healing; endometriosis;
 KW vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
 KW scleroderma, trachoma; vascular adhesion; myocardial angiogenesis;
 KW coronary collateral; cerebral collateral; arteriovenous malformation;
 KW ischaemic limb angiogenesis; Osler-Webber syndrome; wound granulation;
 KW plaque neovascularisation; telangiectasia; haemophilic joint; EST;
 KW angiofibroma; fibromuscular dysplasia; expressed sequence tag;
 KW Crohn's disease; atherosclerosis; birth control; ss.
 XX
 OS Unidentified.
 XX
 PN WO200071577-A1.
 PD 30-NOV-2000.
 XX
 PF 25-MAY-2000; 2000WO-US14462.
 XX
 PR 25-MAY-1999; 99US-0318208.
 PR 20-JUL-1999; 99US-0144882.
 PR 10-AUG-1999; 99US-0147823.
 PR 13-AUG-1999; 99US-0373658.
 PR 22-DEC-1999; 99US-0171503.
 PR 22-FEB-2000; 2000US-0183792.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUB/) RUBEN S M.
 PA (JON/) JONAK Z L.
 PA (TRUL/) TRULLI S H.
 PA (FORN/) FORNWALD J A.
 PA (TERR/) TERRETT J A.
 XX
 XX IrueLA-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH;
 PI Fornwald JA, Terrett JA;
 XX
 DR WPI; 2001-025136/03.
 XX
 XX METH1 and METH2 polynucleotides and encoded polypeptides, used to
 PT inhibit angiogenesis in the treatment of disorders such as cancer,
 PT rheumatoid arthritis and psoriasis -
 XX
 PS Claim 14; Pages 715-718; 768pp; English.
 XX
 CC The present invention relates to human METH1 and METH2, (ME for
 CC metalloproteinase and TH for thrombospondin; see AAB50002 and AAB50003).

CC The present sequence is an expressed sequence tag (EST) for METH. METH
 CC can be used for inhibiting angiogenesis in an individual, and for
 CC treating cancer, benign tumours, an ocular angiogenic disease,
 CC rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis,
 CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
 CC coronary collateral, cerebral collateral, arteriovenous malformations,
 CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC fibromuscular dysplasia, wound granulation, Crohn's disease or
 CC atherosclerosis. METH can also be used in birth control. METH can also
 CC be used in diagnostic methods for the prognosis of cancer.
 XX
 SQ Sequence 5289 BP; 1380 A; 1378 C; 1366 G; 1165 T; 0 other;

Query Match 27.7%; Score 1604.2; DB 22; Length 5289;
 Best Local Similarity 66.1%; Pred. No. 0;
 Matches 2392; Conservative 0; Mismatches 1193; Indels 32; Gaps 4;

QY 152 CTGCGCTTTCTGACTCGGTCCGGAACACTGAAACAGTCACTACATGCTCTTTTGGCA 211
 DB 72 CTGCGCTTTCTGCGCGCGCGCGCGCTGCATCCGCGTCCGACAGGCTCCTTGTGG 131
 QY 212 AACCAAGAGCTCAGTGCAGGAGGAGGATGCTCTGGAGGCTGGTCTGGCTCTGTG 271
 DB 132 CACAATAGCTCCACCATGGGCTGGGCTGGGACTCGGTCTCTCTCTCTCTCTCTGC 191
 QY 272 GGTGGGCGCCACGACGACGCTGGTGCACAGGACAAAGACAGCTTCGACCTTTTTCAG 331
 DB 192 CTGCGCTTCCAAACCCCATCCAGAGTCTGGGGGAGACAAAGTGTGTGACATCTTTGA 251
 QY 332 TATCAGCAACATCAACCGCAAGACCATTTGGCGCCAAAGCAGTTTCCGCGGCGCCAGCCCGG 391
 DB 252 ACTCAGCGGAGCTGCCGCAAGCGTCTGGGCGCGACTGGTGAAGGCGCTGACCCCTC 311
 QY 392 CGTGGCGGCTTACCGCTTCTGGCTTTGACTATACATCCACCGGTGAAGCAGATGACCT 451
 DB 312 TAGCCAGCTTTCCGCTATCGAGGATGCCAACCTGATCCCGCTGTGCTGACAAAGTT 371
 QY 452 CAGCAAGATCACAAGATCATGCGGCAAGAGGAGGCTTCTTCTCAGCGCCACGCTCAA 511
 DB 372 CCAAGACCTAGTGGATGCTGCGGCGGAGAAAGTTTCTCTCTCTCTCTCTCTCTCTG 431
 QY 512 GCAGACGCGCAAGTCCAGGGCACGCTGTGTGGCTCTGGAGGCGCCGCTCTCTCCAGAG 571
 DB 432 GCMAATGAAGAAGACCGCGGTACCTCTGCTGTGGAGCGGAAGACCACTCTGTGCCA 491
 QY 572 GCAGTTCAGATCGTCTCCAAAGGCGCCGCGGACACGCTGGATCTCACCTACTGGATTGA 631
 DB 492 GGTCTTCAGCTGATCTCCAAATGGCAAGGCGGCGCACCTGGACCTGAGCCCTGACCGTGA 551
 QY 632 CGGCACCGGCTATGCTCTCCCTGGAGGAGCTCGGCTCGGTACTCGCAGTGAAGAA 691
 DB 552 GGGGAGCAGCATGTGCTGCGTGGAGAGAGCACTCTCTGGGACTGCCAGTGGAAAG 611
 QY 692 CGTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTGTGACGCTGGGCTCGCACCTATAGG 751
 DB 612 CATACCCCTGTTGTGACAGGAGACAGGCGCCAGCTGTACACTGTGAGAAGATGGA 671
 QY 752 ACCAGTTCCTGGACGAGCCCTTCTACGACACCTGCGAGCGGGAAGAACCCCGATGTA 811
 DB 672 GAATGCGGAGTGGATGTCCCCATCCA-GAGCATCTTCCACCGGAGACCTGCGCAGCATCG 730
 QY 812 CGTGGCCAAAGGCTCTGCGCAGAGAGTGCAC-----TTCAGGGGTTTGTCTCAGAACG 864
 DB 731 CCAGGCTCCGATTTCCCAAGAGAGGTGTCAACGACAAATTTCCAGGGGTGTGTGCAATG 790
 QY 865 TCCACCTAGTGTGAAACCTCTGTGGAAGATATTTCTAAGCAAGAAGGGTTTCCAGCAAG 924
 DB 791 TAAGGTTTGTCTTTGGAACACACACAGAAAGACATCCTCAGGAACAAGGCTGC-----T 844
 QY 925 GCCAGGAGCTGAGATCAACCCCATCAGTGAGAACACAGACGCTGCGCCCTGGTTCGCG 984

Db 845 CCAGCTCTACAGTGTCTTTTGTCAACCTTGCACAAACAGTGGTGAATGGGTCCAGCCCTG 904
QY 985 ATGTCACACCGAGTACGTTGGGCCCCAGCTCGAGAGAGGCCCGAGGTGTGCAAGCCT 1044
Db 905 CCATCCGCACCGACTACATTTGGGCACAAAGAACAAAGGACCTGCAAGCCATCTGTGGCATCT 964
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Db 965 CATGTGACGAGCTGTCCAGCATGGTCTGAGCTCAGGGGTCTACGCACCATCGTGAACA 1024
QY 1105 AGCTACGAGAGAACCTCAAGAGAGTTCGAATGATTAACCAAGTTCTCTGGAGCTCATTTG 1164
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Db 1187 TCTGCAAAAAGTCTCTGTGCCATCATGCCCTGCTCCAAATGCCACAGTTCCGGATGGAG 1246
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Db 1247 AATGCTGCCACGGTGTGCCAGGACTCTGCAGACGATGGTGTGTCCTCCCGTGGTCTG 1306
QY 1405 AGTGGACCAAGTCTCGTCACTGTGGCTCTGGGACCCAGACAGAGGCGGTCTCTGTG 1464
Db 1307 AGTGGACCTCTGCTGTGACCTGTGGCAATGGAATCCAGCAGCGTGGCGCTCCCTGCG 1366
QY 1465 ACCTCAACAGCAACCTCTGGGGCCCTCGATCCAGACAGCGGCTTGCACTGTGACA 1524
Db 1367 ACAGCTCAACACAGATGGAGGGCTCTCTGTGCAGAGCGGACCTGCCACATCCAGG 1426
QY 1525 AGTGTGACACCCGATCCGAGAGCGGCTGGAGCCACTGGTCACTTGGTCTTTCTAT 1584
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QY 1585 GCTCTGTGACCTGTGGAGTTGGCAATATCACAGCATCCGCTCTGCAACTCCCGAGTGC 1644
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QY 1705 CCCATGCCCAATGATGGCGCTGGAGCCCTGGTCCCGCTGGTGGCGCTGCACTGTCA 1764
Db 1607 ACTCTGCCCATCAATGGAGGCTGGGAGCTTGGTCACCATGGAGACTGTCTTCTGTCA 1666
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QY 1825 GAGGAAGGCTGCTGGTGGGATGTGCAGGAGCTGAGATGTGCAACAGAGGAGTGCC 1884
Db 1727 GAGCAAGGACTGCTGGTGGTGTGATGTGACAAAACAGATCTGCAACACAGGACTGTCT 1786
QY 1885 CCGTGGATGGCTGTTTATCAACCCCTGTCTCCGGGAGGCCAGTGCAGAGCTTCCCGG 1944
Db 1787 CCATTGACGATGCTGTCCAATCCCTGCTTGTGTGTCCAGTGTACAGCTACCCCTG 1846
QY 1945 ATGGTCTCTGTCATGGCGCTTCTGCCCTGTGGCTTCTTGGGAATGGCAACCCACTGTG 2004
Db 1847 ATGGCAGCTGGAAAGTGTGGTGCCTGTGCCCGCAGCTATAGTGGAGATGGAGTGCAGTGA 1906
QY 2005 AGGACCTGGAGAGTGTGGCTTGTTCCTCCGACATCTGCTTCTCCACGCAAGTGTGCTC 2064
Db 1907 AAGACGTTGATGAGTGCAAAAGATGCCCTGTGCTCTCAACCAACAAATGGAGACACA 1966

QY 2065 GCTGTGTCAACACTCAGCCTGGCTTCCACTGCTGCTGCCCTCCCGCCCGCCGATACAGAGGA 2124
Db 1967 GGTGTGAGAAACACAGACCCCGCTTACAACTGCTGCTGCCCTCCACCGCTCTCACTGGCT 2026
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Db 2027 CGCAGCCCTTTGGCGGGGCTGGAACATGCCACCCGCAACAGAGGTATGCAAGACCC 2086
QY 2185 AAAACCCATCAAGGACAAGACACACAACTGCCACAAGCAGCGGAGTGCATCTACCTGG 2244
Db 2087 GAAACCCCTGCACAGAGGACACACAGCTGCAACAAGACGCAAGTGCACATCTACCTGG 2146
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Db 2327 AAGACTATGACAAAGGATGGAATCGCGATGCCCTGCGATGATGACGATGACAATGATAAGA 2386
QY 2485 TGACCGATGAGAGGACAACTGCCAGCTCTCTTCAATCCCGCCGAGGCTGACTATGACA 2544
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Db 2567 TCAATGACGGGACAACTGCCAGTATGTCTACAATGTGGACCAAGAAACACTGACATGG 2626
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Db 2627 ACGGGTGTGATCACTGTGACAACTGCCCTTGGAAACAAATCCAGACCAAGCTCAGCT 2686
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QY 2845 ACCAGAACAACAGGACAACTGCCCTTACATCTCCCAACGCCCAACCGGCTGACCATGACA 2904
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Db 2867 GGGACAACCTGCAGCTGGTCCCAATCTTCCAGCAAGGAGCTCTGATGGTGTATGGTCCAG 2926
QY 3025 GTGATATTTTAAAGATGATTTTGACAATGACAACATCCAGATATTTGATGATGTGTGTC 3084
Db 2927 GTGATGTTTCAAGATGATTTTGACCAAGGAGTGGCCAGACATTTGATGATGTGTGTC 2986
QY 3085 CTGAAAACAATGCCATCAGTGAGACAGCTTTCAGGAACTTCCAGATGGTCCCTTGGATC 3144
Db 2987 CCGAAAATGTTGATATCAGTGAGACTGATTTCCCGCGATTCCAGATGATTTCTTCTAGATC 3046

Db 3052 CATCAGGTAAGAACTGTCACAGACTGTCACACTGTCAGCTGCTGAGGTTAT 3111
 QY 3246 GACGAGTTTGGGCTCTGGAGTTTCACTGAGTTCAGTAAACACTGACCGGGACGAC 3305
 Db 3112 GATGAGTTTAAATGCTGGAGTTTCACTGAGTTCAGTAAACACTGACCGGGACGAC 3171
 QY 3306 GACTATGCTGGCTTCTGCTTTGGTTACAGTAAAGCAGCGGCTTCTATGTTGGTGTGG 3365
 Db 3172 GACTATGCTGGATTTCTGCTTTGGCTACCACTCCAGTCCAGACGCGCTTTTATGTTGTGG 3231
 QY 3366 AAGCAGTGCAGGACAGTCTGAGGAGACCAACCCACAGCGGCTTATGCTACTCCGCG 3425
 Db 3232 AAGCAAGTCAACGAGTCTTCTGAGGACCAACCCACAGGAGGCTCAGGAGTACTCGGGC 3291
 QY 3426 GTGTCCTCTCAAGTGTGAATCCACACAGGAGGAGGAGCAGTTCAGGAGACGCGCTG 3485
 Db 3292 CTTTCTGTGAAGTTCTAAATCCACACAGGAGGCTGAGGAGTCTGAGGAGGAGGCTG 3351
 QY 3486 TGCCACAGCGGAGACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3545
 Db 3352 TGCCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3411
 QY 3546 GGTGGAAGGAGTACAGCGCTATAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3605
 Db 3412 GGTGGAAGGAGTACAGCGCTATAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3471
 QY 3606 ATCAGAGTCTTATGATGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3665
 Db 3472 ATTAGAGTGTGATGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3531
 QY 3666 CAACCTACGCTGGGCGGCTGAGTATGCTTCTTCTCAAGAAATGCTATTTTC 3725
 Db 3532 AAACCTATGCTGGTGTAGAGTGGGTTGTTGTTCTCTCAAGAAATGCTTCTTC 3591
 QY 3726 TCAGAGCTCAAGTACGAATGACAGATATTTAAACAGATTTGCTGCAAT 3775
 Db 3592 TCTGACCTGAATACGAATGACAGATATTTAAACAGATTTGCTGCAAT 3641

RESULT 15
 AA232012
 ID AA232012 standard; DNA; 5722 BP.
 XX
 AC AA232012;
 XX
 DT 10-JAN-2000 (first entry)
 XX
 DE Human METH1 related EST X14787.
 DE
 XX
 KW Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
 KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
 KW angiogenesis inhibitor; abnormal wound healing; inflammation;
 KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
 KW diabetic retinopathy; macula degeneration; haemangioma; detection;
 KW arterial-venous malformation; immune deficiency; ss.
 OS
 XX Homo sapiens.
 XX
 PN W09937660-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 22-JAN-1999; 99WO-US01313.
 XX
 PR 23-JAN-1998; 98US-0072298.
 PR 28-AUG-1998; 98US-0098539.
 XX
 XX (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 XX
 PI IrueLA-Arispe L, Hastings GA, Ruben SM;

XX WPI; 1999-590684/50.
 DR New isolated metalloprotease thrombospondin polypeptides, useful for
 XX treating hyperproliferative disorders, cancers or autoimmune disorders
 PT
 PT
 XX Disclosure; Page 252-256; 457pp; English.
 PS
 XX AA232000 and AA232001 encode, and AA49501 and AA49502 represent, human
 CC metalloprotease thrombospondin (METH) proteins METH1 and METH2
 CC respectively. METH1 and METH2 have been found to be potent inhibitors of
 CC angiogenesis both in vitro and in vivo. They can be used for treating
 CC cancer and other disorders related to angiogenesis including abnormal
 CC wound healing, inflammation, rheumatoid arthritis, psoriasis,
 CC endometrial bleeding disorders, diabetic retinopathy, some forms of
 CC macula degeneration, haemangiomas, and arterial-venous malformations.
 CC They may be useful in treating deficiencies or disorders of the immune
 CC system, by activating or inhibiting the proliferation, differentiation,
 CC or mobilisation (chemotaxis) of immune cells. The etiology of these
 CC immune deficiencies or disorders may be genetic, somatic, such as
 CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
 CC toxins), or infectious. They can also be used to treat inflammatory
 CC conditions, both chronic and acute conditions. The products can also be
 CC used for detection and diagnosis. AA232002 to AA232080, and AA49503 to
 CC AA49511 represent sequences given in the exemplification of the present
 CC invention.
 XX Sequence 5722 BP; 1514 A; 1388 C; 1387 G; 1433 T; 0 other;
 SQ
 Query Match 26.8%; Score 1550.4; DB 20; Length 5722;
 Best Local Similarity 65.9%; Pred. No. 0;
 Matches 2326; Conservative 0; Mismatches 1171; Indels 33; Gaps 4;
 QY 252 CTGGTCTCTGGCTGCTGGGTGGCCGACGACGAGCTGGTCCACGAGCAAGAC 311
 Db 139 CTGTTCTTGTATGATGTGTGGACCAACCGCATCCAGAGTCTGGCGGAGACA---AC 195
 QY 312 ACGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGACCTTTGGCCCAAGCAG 371
 Db 196 AGCGTGTGTTGACATCTTTGAACCTACCGGGCGCCGCAAGGGGTCTGGCGCGACTG 255
 QY 372 TTCCGCGGGCGGACCGGGCTGCGGGCTTTACCGCTTCTGCGGCTTTGACTATACATCCCA 431
 Db 256 GTGAAGGGCGCGACCTTCCAGCCGCTTCCGCTGAGGATGCCAACCTGATCCCC 315
 QY 432 CGGTGAACGACGATGACCTCAGCAAGATCACCAGATCATCCGCGCAAGAGGGCTTC 491
 Db 316 CTTGTGCTGATGACAAGTTCCAGACCTGTTGGATGCTGTCGGGCGAGAAAGGTTTC 375
 QY 492 TTCTCTACGGCCGACGCTCAAGCAGGACGCGCAAGTCCAGGGGACGCTGTTGGCTCTGGAG 551
 Db 376 CTCTCTCTGGATCCCTCAGGCAGATGAAGAGACCCGCGGCGACGCTGCTGGCCTGGAG 435
 QY 552 GGCCCGGCTCTCTCCAGAGGAGGATTCGAGATCGTCTCCAAACGGCCCGCGGAGACAGCTG 611
 Db 436 CGGAAGAGACCACTCTGCGCCAGGTCTTCAGCGTGTGTCCAATGGCAAGCGCGGACCTG 495
 QY 612 GATCTCACTACTGATTTGACGGACCGCGCATGTTGCTCCCTGGAGGAGCTGGCGCTG 671
 Db 496 GACCTCACCTGACCGCTCCAGGAAGAGCAGCAGCGTGTGCTGTGGAAGAAGCTCTCTCCTG 555
 QY 672 GCTGACTCGAGTGGAGAAGCTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTTGCAC 731
 Db 556 GCAACCGGCCAGTGGAGAGCATCACCTGTTTGTGCAAGGAAGACAGCGGCCAGCTGTAC 615
 QY 732 GTGGCTCGGACCTCATAGGACAGTCTCTGAGCAGAGCCCTTCTACGAGACCTTCAG 791
 Db 616 ATCGACTGTGAAAGATGGAGAATGCTGAGTTGGACGTCCTCCATCCAAAGGCTCTTACC 675
 QY 792 GCGGAAAGAGCGCGGATGTAGTGGCCAAAGGCTC-----TGGCAGAGAGAGTCTTC 845
 Db 676 AGAGACCTGGCCAGCATGCCAGACTCCGATCCGCAAGAGGGGGCTCAATGACAAATTC 735


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Db 2872 TCTGAGGGCGATGGTGGAGTGATGCTGCAAGATGATTTTGACCATGACAGTGTGCCA 2931
QY 3066 GATATTGATGATGTGTGCTGCTGAAACAAATGCCATCAGTGAGACAGACTTTCAGGAACCTTC 3125
Db 2932 GACATCGATGACATCTGCTGAGAAATGTTGACATCAGTGAGACCGNTTTCGCCGATTC 2991
QY 3126 CAGATGGTCCCTTGGATCCCAAGGGACCCACCAAAATGATCCCAATGGGTCAATCGC 3185
Db 2992 CAGATGATTCCTCTGAGCCCAAGGGACATCCCAAAATGACCTAACTGGGTGTAGCC 3051
QY 3186 CATCAAGCAAGGAGCTGGTTCAGACAGCAACTCGGACCCCGGCATCGCTAGGTTT 3245
Db 3052 CATCAGGTAAAGAACTCGTCCAGACTGTCAACTGTGATCTCGGACTCGCTAGGTTAT 3111
QY 3246 GACGAGTTTGGGTCTGTGACTTTCAGTGGCACATTTCTACGTAAACACTGACCGGGACGAC 3305
Db 3112 GATGAGTTTAAAGTGTGACTTTCAGTGGCACCTTCTTCATCAACACCAAGGAGCGAT 3171
QY 3306 GACTATGCTGGCTTCGTCTTTGGTTACCAAGTCAAGACCGGCTTCTATGTGGTGAATGG 3365
Db 3172 GACTATGCTGGATTTGCTTTGGCTTACCAGTCCAGCAGCCGCTTTATGTTGTGATGG 3231
QY 3366 RAGCAGGTGACGACAGCTACTGGGAGGACCAAGCCACGCGGGGCTATGGCTACTCCGC 3425
Db 3232 AAGCAAGTCAACCCAGCTCTACTGGGACACCAACCCACGAGGGCTCAGGGATACTCGGC 3291
QY 3426 GTGTCCCTCAAGTGGTGAACCTCCACACGCGGGAGCGAGCACCTGAGGAACCGCTG 3485
Db 3292 CTTTCTGTGAAGTTGTAACTCCACACAGGGCTGCGGAGCACCTGCGGAAACGCCCTG 3351
QY 3486 TGGCACACGGGGAACACCGCGGGGAGTGCAGAACCTTTATGSCACGACCCAGGAAACATT 3545
Db 3352 TGGCACACAGGAAACACCCCTGGCCAGCTGGCACCCCTGTGGCATGACCTCGTCACATA 3411
QY 3546 GGCTGGAAGGACTACACGGCCCTATAGGTGGCACCTGACTCAGGCCCAAGACCGGCTAC 3605
Db 3412 GGCTGGAAGATTTCCACCGCCTACAGATGGCGTCTCAGCCACAGGCCAAGACGGGTTTC 3471
QY 3606 ATCAGAGCTTTAGTGCATGAAGGAAACAGGTTCATGGCAGACTCAGGACCTATCTATGAC 3665
Db 3472 ATTAGAGTGGTGATGTAGAGGGNAGAAATCATGGCTGACTCAGGACCCATCTATGAT 3531
QY 3666 CAAACCTAGCTGGGGCGGCTGGGTCTATTGTCTTCTCTCAAGAAATGGTCTATTTC 3725
Db 3532 AAAACCTATGCTGGTGGTAGACTAGGGTTGTTGTCTTCTCTCAAGAAATGGTGTCTTC 3591
QY 3726 TCAGACCTCAAGTACGATGAGAGATATTAAACAGATTTCGTGCATT 3775
Db 3592 TCTGACCTGAATAGAAATGAGAGATCCCTAAATCATCAAAATGTTGATT 3641
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Search completed: December 27, 2002, 00:33:28

Job time : 772 secs

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|-------------------|---------------------|
| | Score | Match | Length | | | |
| 1 | 559.4 | 9.7 | 3074 | 5 | PCN-US93-11725-3 | Sequence 3, Appl1 |
| 2 | 526.4 | 9.1 | 2820 | 5 | PCN-US93-11725-1 | Sequence 1, Appl1 |
| 3 | 255.8 | 4.4 | 1326 | 3 | US-08-985-526-4 | Sequence 4, Appl1 |
| 4 | 252.8 | 4.4 | 657 | 3 | US-08-985-526-2 | Sequence 2, Appl1 |
| 5 | 162.8 | 2.8 | 270 | 1 | US-08-594-031-43 | Sequence 43, Appl1 |
| 6 | 162.8 | 2.8 | 270 | 1 | US-08-594-031-136 | Sequence 136, Appl1 |
| 7 | 162.8 | 2.8 | 270 | 1 | US-08-594-031-143 | Sequence 143, Appl1 |
| 8 | 104.2 | 1.8 | 390 | 4 | US-09-197-649-7 | Sequence 7, Appl1 |
| 9 | 88.6 | 1.5 | 1326 | 4 | US-09-249-585A-4 | Sequence 4, Appl1 |
| 10 | 88.6 | 1.5 | 1931 | 2 | US-09-130-111A-2 | Sequence 2, Appl1 |
| 11 | 64.2 | 1.1 | 5163 | 3 | US-08-700-651-1 | Sequence 1, Appl1 |
| 12 | 64.2 | 1.1 | 5163 | 3 | US-08-928-361B-4 | Sequence 4, Appl1 |
| 13 | 64.2 | 1.1 | 5318 | 3 | US-08-700-651-2 | Sequence 2, Appl1 |
| 14 | 64.2 | 1.1 | 5318 | 3 | US-08-928-361B-3 | Sequence 3, Appl1 |
| 15 | 61.2 | 1.1 | 5311 | 3 | US-08-928-361B-2 | Sequence 2, Appl1 |
| 16 | 61.2 | 1.1 | 7334 | 3 | US-08-928-361B-1 | Sequence 1, Appl1 |
| 17 | 60.2 | 1.0 | 3489 | 2 | US-08-728-323A-1 | Sequence 1, Appl1 |
| 18 | 60.2 | 1.0 | 3489 | 4 | US-09-298-568-1 | Sequence 1, Appl1 |
| 19 | 60.2 | 1.0 | 32207 | 2 | US-08-770-379-20 | Sequence 20, Appl1 |
| 20 | 60.2 | 1.0 | 32207 | 4 | US-08-757-669A-20 | Sequence 20, Appl1 |
| 21 | 60.2 | 1.0 | 32207 | 4 | US-09-230-371A-20 | Sequence 20, Appl1 |
| 22 | 58.4 | 1.0 | 3675 | 4 | US-09-930-872-3 | Sequence 3, Appl1 |
| 23 | 58.4 | 1.0 | 4042 | 4 | US-09-930-872-5 | Sequence 5, Appl1 |
| 24 | 54.2 | 0.9 | 4192 | 4 | US-09-122-126B-1 | Sequence 1, Appl1 |
| 25 | 53.8 | 0.9 | 3624 | 1 | US-07-951-715A-6 | Sequence 6, Appl1 |
| 26 | 53.8 | 0.9 | 3624 | 3 | US-08-459-448A-6 | Sequence 6, Appl1 |
| 27 | 53.8 | 0.9 | 3624 | 3 | US-08-459-595A-6 | Sequence 6, Appl1 |

Db 1295 ATAACATTGGAGATGTTGATGAAGATGCGGATGGAGTGGTATCTTAAATGACGAG 1354
 QY 2500 ACAACTGCCAGCTCTCTTCAATCCCGCCAGCTGACTATGACAAAGGATGAGTTGGG 2559
 Db 1355 ACAACTGTGTGGTGGTCCCAACATCGATCAGAAAAAGTACCAAGATATATTTGGGG 1414
 QY 2560 ACCGTGTGACAGCTGCCCTTACGTGCACAAACCCCTGCCAGTGCACAGACAAAGT 2619
 Db 1415 AGCCCTGTGACAACTGCCCTTAAACCTCAACAATGACCAAGGGGACACAGAAATGACG 1474
 QY 2620 GAGAGGTTGACGCTCTCCGTGGACATTTGATGGGACGATGTCTTCAATGACGAGACA 2679
 Db 1475 GGAAGGAGATGCTTGTGACGATGACATGGATGGATGGCATCAAGATATCTTGGATA 1534
 QY 2680 ATTGTCCTTACGCTTACAACTGACCAAGGACACGAGGATGAGTGTGGGGGATC 2739
 Db 1535 ACTGCCAGAGTTCCCAATGTGGACAGAAAGACAAAGATGGAGTGGTGTGATA 1594
 QY 2740 ACTGTGACAACTGCCCTTGTGTCACAAACCCCTGACCAAGCCGACGACGACGATGCTTTG 2799
 Db 1595 TATGTGACAGCTGTCTTGACATCATATAATCCAAACAGTCAGACATGTGACAATGACCTTG 1654
 QY 2800 TTGGGACCACTGTGTCACAAACAGGACATAGATGACGACGCGCCACCAAGAACCAAGCAG 2859
 Db 1655 TTGGAGATTCCTGTGATACATAACCAAGACAGCGATGGTGTGCTACAGGACAGCACAG 1714
 QY 2860 ACAACTGCCCTTACATCTCCAAAGCCCAACAGCTGACCATGACAGAGACGCGGCGG 2919
 Db 1715 ACAACTGCCCACTGATGATAACAGCAACAGCAGCTGACACAGCAAGGACGCGCATGGAG 1774
 QY 2920 AGCCCTGTGACCTGATGATGACAAAGATGGGTGCTCCCAT-----GACAGG 2967
 Db 1775 ATGAATGTGACGATGATGATGAAGATGGAATCCCGGATACTGTCTCCCGGACCTTG 1834
 QY 2968 ACAACTGCCGCTGTGTTCACACCCAGCAGGAGACTTGGACGCTGATGACGCGGTG 3027
 Db 1835 ATAACGTAACTGTGTTCACACCCAGGCGAGGAGTGCACACATGATGAGTGGAG 1894
 QY 3028 ATATTGTAAAGATGATTTGACATGACAAATCCAGATATGATGATGATGATGATGATG 3087
 Db 1895 AGCTGTGTGAGCCGATTTTGTACAGGACAGCTGATGACCGAATTTGACGCTTGGCCTG 1954
 QY 3088 AAAACAATGCCATCAGTGAGACAGACTTCAGGAACCTTCAGATGTCCTTGGATCCCA 3147
 Db 1955 AAAATGCAGAGATCACCTTGACAGATTTTCCAGAGCTTATCAAACCTGTAGTTGGATCCCG 2014
 QY 3148 AAGGGACCAACCAAAATGATCCCACTGGGTGATTCGCCATCAAGCAAGAGCTGGTTC 3207
 Db 2015 AAGGAGATGCCCAAAATGATCCAACTGGATTTGTTGAACAGGAATGGAGATTGTGC 2074
 QY 3208 AGACAGCAACTCGGACCCCGGATCGCTGTAGGTTTGAAGTTTGGGTCTGTGGACT 3267
 Db 2075 AGACATGAACAGTACCTCGGCTGACGAGTGGTGTACACAGCATTAATGAGTTGAT 2134
 QY 3268 TCAGTGGCAGATTCACGTAAACACTGACCGGACGACACTATGCTGCTGCTTTG 3327
 Db 2135 TCAGGGGCACATTCACGTGAACACCATGACCGGATGATGATTACCGTGTTCATCTTG 2194
 QY 3328 GTTACAGTCAAGCAGCCCTTCTATGTGTGATGTTGGAAGCAGGTGACGACACTACT 3387
 Db 2195 GTTATCAGGACATTCACACTTTTATGTGTGATGTTGGAAGCAGACTGACGACTTACT 2254
 QY 3388 GGGAGACAGCCGACGCGGCTATGGCTATCCGGCTGTCCCTCAAGGTTGGTGAAT 3447
 Db 2255 GCGAGCAACCCCTTCAGACGAGTGTGACAGCTTGAATCCAACTGAAGGCTGTCAAT 2314
 QY 3448 CCACACGGGGAGCGGACGACCTGAGGAACCGCTGTGGGACACGCGGACACCCCG 3507
 Db 2315 CCAAGTCAGGACCGGGGAACATCTGAGGAACGCTGTGGGACACAGGAGACACCAATG 2374
 QY 3508 GCGAGTGGGAACCTTATGGCAGCAGCCCGAGGAACATTTGGCTGGAGGAGTACACGGCT 3567
 Db 2375 ATCAAGTGAAGCTGCTCTGGAAGACCCCGAGGATGTCGGCTGGAAGAACAAAGTCTCT 2434

RESULT 3

US-08-985-526-4
 ; Sequence 4, Application US/08985526
 ; Patent No. 6080728
 ; GENERAL INFORMATION:
 ; APPLICANT: Mixson, James A
 ; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
 ; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
 ; TITLE OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
 ; STREET: 1220 Market Street, P.O. Box 2207
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: U.S.A.
 ; ZIP: 19899
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/985,526
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/608,845
 ; FILING DATE: 16-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMorow Jr., Robert G
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 658-9141
 ; TELEFAX: (302) 658-5613
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1326 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-985-526-4

Query Match 4.48; Score 255.8; DB 3; Length 1326;
 Best Local Similarity 64.7%; Pred. No. 1.1e-51;
 Matches 380; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
 QY 1225 AAAATCAACGTTGGTGGACAGCTGCACACGCTGTACTCCAGAAATTTAAACCA 1284
 Db 80 ATACAGGAATGGACTGTGTGATGCTGACTGAGTGTCTGACAGACTAGTTACCA 139
 QY 1285 TTTCGCCCAAAATCACTGCCCCCTGCACACCTGCCCGAGTCCATCCTTTGTGGAAGCG 1344
 Db 140 TCTGCAAAAAGGTGCTCTGCCCATCATGCCCCATGCTGCTTCCCAATGCCACAGTTCCTGATGGAG 199
 QY 1345 AATGCTGCCCTTCTCTGCCCTCCACTCGGTGACCGTGAGGAGGCTGGTCTCCTGGGCGAG 1404

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Db 200 AATGCTGCTCGTGTGGCCAGCGACTCTGGGAGGATGGCTGCTCCATGGTCCG 259
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Qy 1525 AGTGACACCCGATCCGGCAGCAGCGGCTGGAGCCCTGAGCCACTGTCTACCTTGTCTCAT 1584
Db 380 AGTGACAAAGATTTAAACAGGATGTGCTGGAGCCACTGTCTCCCGGTGCTACTT 439
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Qy 1645 CCCAGATGGGGGCAAGATTTGCAAGGAGTGGCCGGGAGACCAAGCCCTGCCAGGCG 1704
Db 500 CCCAGATGAATGGGAACCCCTGTGAAGCGAAGCGCGGAGACCAAGCCCTGCCAAGAA 559
Qy 1705 CCCATGCCAATCGATGGCGCTGGAGCCCTGCTGCTCCCGTGTGGCTGCACTGTCA 1764
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Qy 1765 CTTGTGCGGTGGATCCGGGAGCGCACCCCGGTCTGCAACAGCCCT 1811
Db 620 CTTGTGGAGGAGGGGTACAGAAACGTAGTCTGCTGCTGCTGCT 666

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RESULT 4

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US-08-985-526-2
; Sequence 2, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorro Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 657 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-526-2

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Query Match 4.4%; Score 252.8; DB 3; Length 657;
Best Local Similarity 64.9%; Pred. No. 4.1e-51;
Matches 374; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
Qy 1225 AAATGAACACGTGGTGGACAGCTGCCACACGTGTACCTGCAAGAAATTTAAACCA 1284
Db 80 ATAAACAGGAATGACTGTTGATAGCTGCACTGAGTGTCTACTGTGACAGAACTCAGTTACCA 139
Qy 1285 TTTCGCCAAATCACCTGCGCCGCTGCAACCTGCGCCAGTCCATCTTTGTGGAAGCG 1344
Db 140 TCTGCAAAAGGTGCTCTGCCCCATATGCCCTGCTTCAATGCCACATTTCTGATGGAG 199
Qy 1345 AATGCTGCCCTTCTGCTCCACTCGGTGGAGCGGTGAGAGGGCTGTCTCCGTGGGCGAG 1404
Db 200 AATGCTGTCTCTGCTGTTGGCCAGCGACTCTGCGGAGGATGGTGTCTCCATGGTCCG 259
Qy 1405 AGTGACCCAGTGTCTCGTGTGCTGTGGAGCCAGAGAGCGCGGTCTGTG 1464
Db 260 AGTGACCTCTCTGTTCTACGAGCTGTGGCAATGGAATTCAGACGCGCGCGCTCTCG 319
Qy 1465 ACGTACACAGCAACACCTGCTTGGGGCCCTCGATCCAGACACGGCTTGCAGTCTGAGCA 1524
Db 320 ATAGCCTCAACACCGATGTGAGGGCTCTCGTCCAGACAGGACCTGCCACATTCAGG 379
Qy 1525 AGTGACACCCGATCCGGCAGCAGCGGCTGTGAGCCACTGTGCTACCTTTGGTCTTCA 1584
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Qy 1585 GCTCTGTGACCTGTGGAGTTGGCAATATCACACGATCCGCTCTGCAACTCCCGAGTGC 1644
Db 440 GTTCTGTGACATGTGTGATGTGTATCACAAGGATCCCGCTCTGCAACTTCTCCAGCC 499
Qy 1645 CCCAGATGGGGCAAGATTTGCAAGGAGTGGCGGAGACCAAGCCCTGCCAGGCG 1704
Db 500 CCCAGATGAATGGGAACCCCTGTGAAGCGAAGCGCGGAGACCAAGCCCTGCCAAGAA 559
Qy 1705 CCCATGCCAATCGATGGCGCTGGAGCCCTGCTGCTCCCGTGTGGCTGCACTGTCA 1764
Db 560 ACGCTGCCCATCAATGGAGGCTGGGCTCTGTGTCACCATGGAGATCTGTCTGTCA 619
Qy 1765 CTTGTGCGGTGGATCCGGGAGCGCACCCCGGTCT 1800
Db 620 CTTGTGGAGGAGGGGTACAGAAACGTAGTCTGCTCT 655

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RESULT 5

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US-08-594-031-43
; Sequence 43, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995

```


ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
J5-OR-594-031-136

| Query Match | 2.88; | Score 162.8; | DB 1; | Length 270; |
|-----------------------|---|------------------|-----------|-------------|
| Best Local Similarity | 87.6%; | Pred. No. 1e-29; | | |
| Matches 212; | Conservative 0; | Mismatches 27; | Indels 3; | Gaps 3; |
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| Db 6 | AGGTCCGGACTATGGCATGACCCCAAAACATTTGGCTGGAAAGATTACACTGCCCTACA | 65 | | |
| QY 3571 | GGTGGCACCTGACATCAGAGGCCCAAGACCGGCTACATCAGAGTCTTATGTCATGAAGGAA | 3630 | | |
| Db 66 | GGTGGCACCTGATTCACAGGCCTAAGACAGGCTACATGAGAGTCTTATGTCATGAAGGAA | 125 | | |
| QY 3631 | AACAGGTGTCATGGCAGACTCAGGACCTATCTATGACCAAAACCTACGCTGGCGGGCGGTGG | 3690 | | |
| Db 126 | AGCAAGTCATGGCTGACTCAGGACCAATTTATGACCAAAACCTACGCTGGTGGACGGCTGG | 185 | | |
| QY 3691 | GTCTATTATGCTTCTCTCAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCAGAG | 3750 | | |
| Db 186 | G-CGTGTTGTGTTCTC-CAAGAGATGGTCTA-TTCTCGGACCTCAAGTATGATGTCAGAG | 242 | | |
| QY 3751 | AT 3752 | | | |
| Db 243 | AT 244 | | | |

RESULT 7
US-08-594-031-143
; Sequence 143, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-143

Query Match 2.8%; Score 162.8; DB 1; Length 270;
Best Local Similarity 87.6%; Pred. No. 1e-29;
Matches 212; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

QY 3511 AGGTGCGAACCTTATGGACAGCCAGACATTGGCTGGAAGACTACAGGCGCTATA 3570
DB 6 AGGTGCGGACTCTATGGCATGCCCAAAACATTGGCTGGAAGATTACACTGCTACA 65
QY 3571 GTGTCACCTGACTCAGACAGCCAGACCGCTACATCAGAGTCTTAGTGATGAAGAA 3630
DB 66 GTGTCACCTGATTCAGAGGCTTAGACAGGCTAGATGAGAGTCTTAGTGATGAAGAA 125
QY 3631 AACAGGTCATGCGACACTCAGGACCTATCTATGACAAACCTACGCTGGCGGCGCTGG 3690
DB 126 AGCAAGTCACTGGCTGACTCAGGACCAATTTATGACAAACCTACGCTGGCGGCTGG 185
QY 3691 GTCTATTGCTCTCTCAAGAAATGGTCTATTCTTCAGACCTCAAGTACGAATGCGAG 3750
DB 186 G-CTGTTGTTCTTCTC-CAAGAGATGGTCTA-TTCTCGGACCTCAAGTATGATGTCAGAG 242
QY 3751 AT 3752
DB 243 AT 244

RESULT 8
US-09-197-649-7
Sequence 7, Application US/09197649
Patent No. 6194550
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Pribnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/CI-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER FILING DATE: 1997/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER FILING DATE: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence

OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
US-09-197-649-7
OTHER INFORMATION: fragments having NcoI restriction sites.

Query Match 1.8%; Score 104.2; DB 4; Length 390;
Best Local Similarity 55.0%; Pred. No. 1.4e-15;
Matches 205; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 2595 GCGGATCGACACAGACAATGGAGAGGTGAGCGCTGCTCGTGACATTTGATGGG 2654
DB 3 GCGGATCGACACAGACAATGGAGAGGTGAGCGCTGCTCGTGACATTTGATGGG 52
QY 2655 GACGATGCTTCAATGAGAGAGACAATTTGCTTACGCTTACAACTGACAGAGGAC 2714
DB 63 GACGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 122
QY 2715 ACGGATGCTGAGGCTGCTGAGGATGCTGACAACTGCTGACAACTGCTGCTGCTGAC 2774
DB 123 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182
QY 2775 CAGACCGACGCTGGACAATGACCTTTGTTGGGACCACTGTGACAACTGACATAGAT 2834
DB 183 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
QY 2835 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2894
DB 243 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 302
QY 2895 GACCATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2954
DB 303 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 362
QY 2955 CCCGATGACAGGG 2967
DB 363 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375

RESULT 9
US-09-249-585A-4/c
Sequence 4, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISODES
FILE REFERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

Query Match 1.5%; Score 88.6; DB 4; Length 1926;
Best Local Similarity 47.3%; Pred. No. 1.9e-11;
Matches 302; Conservative 0; Mismatches 334; Indels 3; Gaps 1;

QY 2418 GCGCAGGAAGACTTTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2477
DB 961 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 902
QY 2478 GACGGTGTGACCGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2537
DB 901 GACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842
QY 2538 TATCAGAGGATGAGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2597

Db 841 GACGAGGACGGGAGGACGGGAGGAGGACGAGGACGGGAGGACGGGAGGACGAGGAC 782
Qy 2598 CAGATCAGACAGACACAAATGAGAGGGTGACGCCCTGCTCGCTGGACATTTGATGGGAC 2657
Db 781 GGGGAGGACGGGAGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACG 722
Qy 2658 GATGCTTTCATTAACAGAGCAATTTGTCCTTACCTTACACACTGACCACTGACCACTGAC 2717
Db 721 GACGGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGAGGACGGGAGGAGGAG 662
Qy 2718 GATGGTGACGGTGTTGGGGATCACTGTGACAACTGTCGACAACTGTCGACAACTGTCGAC 2777
Db 661 GACGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAG 602
Qy 2778 ACCGACGTGGACAATGACCTTTGTTGGGACCACTGTGACAACTGTCGACAACTGTCGAC 2837
Db 601 GAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAG 542
Qy 2838 GACGCCACCAAGACACACGAGGACAACTGCCCTTACATCTCCAACGCCAACGAGCTGAC 2897
Db 541 GGGGAGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGAGGACGGGAGGAGGAG 482
Qy 2898 CATGACAGAGACGGGACGGGACGGCTGTGACCCCTGATGATGACAACTGTCGACAACT 2957
Db 481 GAGGACGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAG 422
Qy 2958 GATGACAGGACAACTGCCGCTTGTCTTCAACCCAGACGAGGAGGACTTGGACGGTGAT 3017
Db 421 GAGGACGGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAGGAGGAG 365
Qy 3018 GGACGGGTGATATTGTTAAAGATGATTTTGAACAATGAC 3056
Db 364 GACGGGAGGACGGGAGGAGGACGGGAGGAGGACGAGGACGAGGAC 326

RESULT 10

US-09-130-114-2/c

; Sequence 2, Application US/09130114

; Patent No. 5978807

; GENERAL INFORMATION:

; APPLICANT: Horlick, Robert A.

; APPLICANT: Damaj, Bassam B.

; APPLICANT: Robbins, Alan K.

; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes

; TITLE OF INVENTION: From Multiple Transfected Episomes

; FILE REFERENCE: 0867/1D903051

; CURRENT APPLICATION NUMBER: US/09/130,114

; CURRENT FILING DATE: 1998-08-06

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 1931

; TYPE: DNA

; ORGANISM: EBNA

US-09-130-114-2

Query Match 1.5%; Score 88.6; DB 2; Length 1931;
Best Local Similarity 47.3%; Pred. No. 1.9e-11;
Matches 302; Conservative 0; Mismatches 334; Indels 3; Gaps 1;

Qy 2418 GGGCAGGAGACTTTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2477
Db 961 GAGGACGAGGACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 902
Qy 2478 GACGGTGACCGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2537
Db 901 GACGGGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842
Qy 2538 TATGACAAGGATAGGTTGGGGACCGCTGTGACAACTGCCCTTACGTGACAACTGCCCTGCC 2597
Db 841 GACGAGGACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 782
Qy 2598 CAGATCAGACAGACAAATGAGAGGGTGACGCCCTGCTCGCTGGACATTTGATGGGAC 2657

Db 781 GGGGAGGACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722
Qy 2658 GATGCTTTCATTAACAGGAGCAATTTGTCCTTACCTTACACACTGACCACTGACCACTGAC 2717
Db 721 GACGGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGAGGACGGGAGGAGGAGGAG 662
Qy 2718 GATGGTGACGGTGTTGGGGATCACTGTGACAACTGTCGACAACTGTCGACAACTGTCGAC 2777
Db 661 GACGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAGGAG 602
Qy 2778 ACCGACGTGGACAATGACCTTTGTTGGGACCACTGTGACAACTGTCGACAACTGTCGAC 2837
Db 601 GAGGAGGACGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAGGAGGAGGAG 542
Qy 2838 GACGCCACCAAGACACACGAGGACAACTGCCCTTACATCTCCAACGCCAACGAGCTGAC 2897
Db 541 GGGGAGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGAGGACGGGAGGAGGAG 482
Qy 2898 CATGACAGAGACGGGACGGGACGGCTGTGACCCCTGATGATGACAACTGTCGACAACT 2957
Db 481 GAGGACGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAG 422
Qy 2958 GATGACAGGACAACTGCCGCTTGTCTTCAACCCAGACGAGGAGGACTTGGACGGTGAT 3017
Db 421 GAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGACGGGAGGAGGAGGAGGAGGAG 365
Qy 3018 GGACGGGTGATATTGTTAAAGATGATTTTGAACAATGAC 3056
Db 364 GACGGGAGGACGGGAGGAGGACGGGAGGAGGACGAGGACGAGGAC 326

RESULT 11

US-08-700-651-1

; Sequence 1, Application US/08700651B

; Patent No. 6015882

; GENERAL INFORMATION:

; APPLICANT: PETERSEN, CAROLYN

; APPLICANT: LEECH, JAMES

; APPLICANT: NELSON, RICHARD, C.

; APPLICANT: GUT, JIRI

; TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS

; TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum

; TITLE OF INVENTION: INFECTIONS

; FILE REFERENCE: 480.19-4(HV)

; CURRENT APPLICATION NUMBER: US/08/700,651B

; CURRENT FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: 08/415,751

; EARLIER FILING DATE: 1995-04-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 5163

; TYPE: DNA

; ORGANISM: Cryptosporidium parvum

US-08-700-651-1

Query Match 1.1%; Score 64.2; DB 3; Length 5163;
Best Local Similarity 43.7%; Pred. No. 2.4e-05;
Matches 282; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

Qy 2265 TACAAGTGCAGTGCAGACAGGCTACCGGGCGGACGGGCTCATCTGCGGGGAGGACTCG 2324
Db 553 TAAATGTGTTGAGTGAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 612
Qy 2325 GACCTGGACGGCTGCCCAACCTCAATCTGTCGCGCCCAACCAACCCACCTACCACTGC 2384
Db 613 GACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 672
Qy 2385 ATCAAGGATAACTGCCCCCATCTGCCAAATTTCTGGGCGAGGAAGACTTTTGACAAGGACGG 2444
Db 673 GACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 732

| | | | |
|----|------|---|------|
| QY | 2865 | TGCCCCTACATCTCCAACGCCCAACCAGGCTGACCATGACAGAGAC | 2909 |
| | | - - - - - | |
| Db | 1152 | AACAACACTACTACTACTACTACAACCCAGAAACCAACAACAACACTAC | 1196 |

RESULT 15

```

US-08-928-361B-2
: Sequence 2, Application US/08928361B
: Patent No. 6071518
: GENERAL INFORMATION:
: APPLICANT: Petersen, Carolyn
: TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
: TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
: TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
: TITLE OF INVENTION: SPECIES INFECTIONS
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PETERS, VERNY, JONES & BIKSA
: STREET: 385 Sherman Avenue, Suite 6
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306-1840
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/928,361B
: FILING DATE: 12-SEP-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/026,062
: FILING DATE: 13-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Verny, Hana
: REGISTRATION NUMBER: 30,518
: REFERENCE/DOCKET NUMBER: 480.76-1(HV)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-324-1677
: TELEFAX: 650-324-1678
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5511 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-928-361B-2

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| Query Match | 1.1% | Score 61.2; | DB 3; | Length 5511; |
|-----------------------|--------------------|---------------------|--------------------------------------|--------------|
| Best Local Similarity | 45.3% | Pred. No. 0.00013; | | |
| Matches 222; | Conservative 0; | Mismatches 268; | Indels 0; | Gaps 0; |
| QY 2487 | ACCGATGAGGAGGACAAC | TGCCACGCTCCTCTTCAAT | CCCCCGCAGGTGACTATGACAAG | 2546 |
| | | | | |
| DB 927 | AACAACAACAACAAC | TACTACTACTACGACAACA | CAACAACAACGACACAAC | 986 |
| | | | | |
| QY 2547 | GATGAGGTGGGGACCG | GTGACAACCTTACGTCG | TGCACACCCCTGCCACGATGCAC | 2606 |
| | | | | |
| DB 987 | AACAACAAC | TACTACAACTACTACCA | CTACTACTACGACACACAACTACTACTACGAC | 1046 |
| | | | | |
| QY 2607 | ACAGACAACAATGGAG | GGGTGAGCGCTGCTCG | TGGACATGTATGCGGACGATGTCCTC | 2666 |
| | | | | |
| DB 1047 | AACAACAACAACAAC | TACTACTACTATAAAC | CACAAACAACTACAACCGACGAACTAC | 1106 |
| | | | | |
| QY 2667 | AATGAACGAGACAA | TGTCCCTACGCTGTACA | AACTACTGACAGAGGACACGGATGGTGAC | 2726 |
| | | | | |
| DB 1107 | AACCCACAACCACTAC | CAAGAAACCAACAACA | CAACAACAACAACAACAACAACAACAACA | 1166 |
| | | | | |
| QY 2727 | GGTGTGGGGGAT | CTCTGTGACAAC | TGCCCTGTGTGCACAACCCCTGACCAAGACGACGTG | 2786 |
| | | | | |

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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:20:19 ; Search time 181 Seconds
(without alignments)
12981.546 Million cell updates/sec

Title: US-09-919-770-3
Perfect score: 5784
Sequence: 1 accgcatccagtcacagagg.....aattgtaaaagggtttct 5784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|----|---------------------|
| 1 | 5784 | 100.0 | 5784 | 10 | US-09-919-770-3 |
| 2 | 5784 | 100.0 | 5784 | 10 | US-09-880-107-2160 |
| 3 | 3683.4 | 63.7 | 3787 | 10 | US-09-925-301-189 |
| 4 | 3573.6 | 61.8 | 3596 | 10 | US-09-822-682-1 |
| 5 | 1550.4 | 26.8 | 5722 | 10 | US-09-880-107-3701 |
| 6 | 1548.8 | 26.8 | 7231 | 10 | US-09-919-172-64 |
| 7 | 1529.8 | 26.4 | 5830 | 10 | US-09-925-301-205 |
| 8 | 601.6 | 10.4 | 2439 | 9 | US-09-954-531-140 |
| 9 | 601.6 | 10.4 | 2439 | 9 | US-09-954-531-359 |
| c 10 | 595.6 | 10.3 | 619 | 9 | US-10-025-380-327 |
| c 11 | 595.6 | 10.3 | 619 | 10 | US-09-922-217-327 |
| c 12 | 595.6 | 10.3 | 619 | 10 | US-09-833-263-327 |
| c 13 | 540.2 | 9.3 | 637 | 10 | US-09-815-343-1448 |
| c 14 | 516 | 8.9 | 516 | 10 | US-09-920-300A-1233 |
| c 15 | 516 | 8.9 | 516 | 12 | US-10-033-528-1233 |
| c 16 | 514.6 | 8.9 | 925 | 10 | US-09-919-603-6 |
| c 17 | 423.6 | 7.3 | 435 | 9 | US-09-736-457-592 |
| c 18 | 423.6 | 7.3 | 435 | 9 | US-09-902-941-592 |
| c 19 | 423.6 | 7.3 | 435 | 9 | US-09-604-287A-223 |

| | | | | | | |
|------|-------|-----|------|----|---------------------|--------------------|
| 20 | 407.8 | 7.1 | 411 | 10 | US-09-339-338-223 | Sequence 223, App |
| 21 | 407.8 | 7.1 | 411 | 12 | US-10-007-805-223 | Sequence 223, App |
| c 22 | 370 | 6.4 | 478 | 10 | US-09-815-343-834 | Sequence 834, App |
| 23 | 335.4 | 5.8 | 486 | 10 | US-09-925-299-478 | Sequence 478, App |
| 24 | 332.2 | 5.7 | 438 | 10 | US-09-833-381-1864 | Sequence 1864, App |
| c 25 | 319.6 | 5.5 | 390 | 10 | US-09-954-456-785 | Sequence 785, App |
| c 26 | 319.6 | 5.5 | 390 | 10 | US-09-880-107-1916 | Sequence 1916, App |
| c 27 | 300 | 5.2 | 300 | 10 | US-09-815-343-508 | Sequence 508, App |
| 28 | 252.8 | 4.4 | 1326 | 12 | US-10-036-869-2 | Sequence 4, Appli |
| 29 | 252.8 | 4.4 | 1326 | 12 | US-10-036-869-2 | Sequence 2, Appli |
| 30 | 179 | 3.1 | 755 | 10 | US-09-919-603-4 | Sequence 4, Appli |
| 31 | 114 | 2.0 | 614 | 10 | US-09-815-343-612 | Sequence 612, App |
| 32 | 108.6 | 1.9 | 255 | 10 | US-09-925-301-781 | Sequence 781, App |
| 33 | 104.2 | 1.8 | 390 | 10 | US-09-790-399-7 | Sequence 7, Appli |
| c 34 | 100.6 | 1.7 | 312 | 9 | US-09-736-457-952 | Sequence 952, App |
| c 35 | 100.6 | 1.7 | 312 | 9 | US-09-902-941-952 | Sequence 952, App |
| c 36 | 98.8 | 1.7 | 406 | 10 | US-09-960-352-8997 | Sequence 8997, App |
| 37 | 98.2 | 1.7 | 2596 | 10 | US-09-764-853-380 | Sequence 380, App |
| 38 | 98.2 | 1.7 | 2596 | 10 | US-09-764-898-128 | Sequence 128, App |
| c 39 | 91.2 | 1.6 | 408 | 10 | US-09-960-352-7596 | Sequence 56, Appl |
| c 40 | 89.6 | 1.5 | 392 | 10 | US-09-960-352-260 | Sequence 7596, App |
| c 41 | 89.6 | 1.5 | 392 | 10 | US-09-960-352-260 | Sequence 260, App |
| c 42 | 89.6 | 1.5 | 439 | 10 | US-09-960-352-3062 | Sequence 3062, App |
| c 43 | 88.4 | 1.5 | 428 | 10 | US-09-960-352-10669 | Sequence 10669, A |
| c 44 | 88 | 1.5 | 2820 | 10 | US-09-854-845-15 | Sequence 15, Appl |
| 45 | 88 | 1.5 | 2865 | 10 | US-09-854-845-13 | Sequence 13, Appl |

ALIGNMENTS

RESULT 1

US-09-919-770-3
; Sequence 3, Application US/09919770
; Patent No. US20020048577A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, Paul
; APPLICANT: Kyriakides, Themis
; APPLICANT: Ratner, Buddy
; APPLICANT: Glachelli, Cecilia
; APPLICANT: Martinson, Laura
; APPLICANT: Scatena, Marta
; TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
; FILE REFERENCE: UOFW117618
; CURRENT APPLICATION NUMBER: US/09/919,770
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,071
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240)..(3755)
US-09-919-770-3

| | | | | |
|-----------------------|-----------------|---|-----------|--------------|
| Query Match | 100.0% | Score 5784; | DB 10; | Length 5784; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 5784; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | ACGGCATCAACACCGCGCTGCCCGGAGCCGCTGGCCACGTCACAGCCCTGCACAGGAGAG 60 | | |
| Db | 1 | ACGGCATCAACACCGCGCTGCCCGGAGCCGCTGGCCACGTCACAGCCCTGCACAGGAGAG 60 | | |
| Qy | 61 | CGGCATATAAAGCGCGCTGCCCGGAGCCGCTGGCCACGTCACAGGAGAGAGAGAGAGAG 120 | | |
| Db | 61 | CGGCATATAAAGCGCGCTGCCCGGAGCCGCTGGCCACGTCACAGGAGAGAGAGAGAGAG 120 | | |
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| Db | 121 | CTGAGGCGCGGTCTCTCGCTCCAGCAGCGCTGGCGCTTCTGACTCGTCCGGAACAC 180 | | |

Db 121 CTGACGGCGGGTCTCTGGCTCAGCAGAGCCCTGGCCCTTTCTGACTCGGTCCGGAAACAC 180
QY 181 TGAACACAGTCATCACTGATCTTTTTTGGCAACACAGGAGCTCAGCTGCAGGAGGCAGGA 240
Db 181 TGAACACAGTCATCACTGATCTTTTTTGGCAACACAGGAGCTCAGCTGCAGGAGGCAGGA 240
QY 241 TGGTCTGGAGGCTGGTCTCTGCTGGCTCTGTGGGTGTGGGCTGAGCCAGCAGCAAGCTGGTCAAC 300
Db 241 TGGTCTGGAGGCTGGTCTCTGCTGGCTCTGTGGGTGTGGGCTGAGCCAGCAGCAAGCTGGTCAAC 300
QY 301 AGGACAAGACAGCAGCTTTCAGCTTTTTCAGTATCAGCAACATCAACCCGCAAGACCATG 360
Db 301 AGGACAAGACAGCAGCTTTCAGCTTTTTCAGTATCAGCAACATCAACCCGCAAGACCATG 360
QY 361 GCCCCAAGCAGTTCCCGGGGCCGACCCCGGGCTGCGGGCTTACCGCTTTCGTCGCTTTG 420
Db 361 GCSCCAAGCAGTTCCCGGGGCCGACCCCGGGCTGCGGGCTTACCGCTTTCGTCGCTTTG 420
QY 421 ACTACATCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCAGATCATCGGSCAGA 480
Db 421 ACTACATCCACCGGTGAACGCAGATGACCTCAGCAAGATCACCAGATCATCGGSCAGA 480
QY 481 AGGAGGCTTCTTCTCAGCGGCCAGCTCAAGCAGGACGCAAGTCCAGGGCACGCTCT 540
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QY 541 TGGCTCTGGAGGGCCCGGCTCTCTCCAGAGGAGCTTCAGAGATCGTCTCCAACGGGCCCG 600
Db 541 TGGCTCTGGAGGGCCCGGCTCTCTCCAGAGGAGCTTCAGAGATCGTCTCCAACGGGCCCG 600
QY 601 CGGACACGCTGATCTCACTACTGATTTGAGGGCACCCCGGATGTTGTTCCCTGGAGG 660
Db 601 CGGACACGCTGATCTCACTACTGATTTGAGGGCACCCCGGATGTTGTTCCCTGGAGG 660
QY 661 AGCTCGGCTTGGTACTCGAGTGAAGAACGTCACCGTCAGGTTGGCTGCGGAGACCT 720
Db 661 AGCTCGGCTTGGTACTCGAGTGAAGAACGTCACCGTCAGGTTGGCTGCGGAGACCT 720
QY 721 ACAGCTTGACGCTGGGCTCGGACCTCATAGGACCAAGTTCCTCTGGACGAGCCCTTCTAG 780
Db 721 ACAGCTTGACGCTGGGCTCGGACCTCATAGGACCAAGTTCCTCTGGACGAGCCCTTCTAG 780
QY 781 AGCAGCTGACGGGGAAGAGCCGGATGATGTCGCGCAAGAGGCTCTGCCAGAGAGTTC 840
Db 781 AGCAGCTGACGGGGAAGAGCCGGATGATGTCGCGCAAGAGGCTCTGCCAGAGAGTTC 840
QY 841 ACTTCAGGGCTTGGTTTCAGAACGCTCCACCTAGTGTGTTTGAAGTCTGTGGAAGATATTC 900
Db 841 ACTTCAGGGCTTGGTTTCAGAACGCTCCACCTAGTGTGTTTGAAGTCTGTGGAAGATATTC 900
QY 901 TAAGCAAGAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCATCAGTGAACA 960
Db 901 TAAGCAAGAGGTTGCCAGCAAGGCCAGGGAGCTGAGATCAACGCCATCAGTGAACA 960
QY 961 CAGAGACGCTGGCCCTGGTCCGATGTACACACGAGTACGTGGGCCCGGACGCTCGGAGA 1020
Db 961 CAGAGACGCTGGCCCTGGTCCGATGTACACACGAGTACGTGGGCCCGGACGCTCGGAGA 1020
QY 1021 GGAGGCCGAGGTGTGCAAGCCTCGTGGAGGAGCTGSGAAACATGTTCCAGGAGCTCT 1080
Db 1021 GGAGGCCGAGGTGTGCAAGCCTCGTGGAGGAGCTGSGAAACATGTTCCAGGAGCTCT 1080
QY 1081 CGGGCTCCACGCTCTCTGTAACACGCTCAGCGAGAACCTCAAGAGAGTGTGGAATGATA 1140
Db 1081 CGGGCTCCACGCTCTCTGTAACACGCTCAGCGAGAACCTCAAGAGAGTGTGGAATGATA 1140
QY 1141 ACCAGTTCTCTGGAGCTCATTTGTTGGCTTCTTAAGACAGGAACATGTCAGCTTGT 1200
Db 1141 ACCAGTTCTCTGGAGCTCATTTGTTGGCTTCTTAAGACAGGAACATGTCAGCTTGT 1200
QY 1201 GGCAGGATGGCGGTTCTTTGGGGAATGAAACGTTGGTGGAGACGCTGCACACGCT 1260
Db 1201 GGCAGGATGGCGGTTCTTTGGGGAATGAAACGTTGGTGGAGACGCTGCACACGCT 1260

QY 1261 GTACCTGCAAGAAATTTAAACCATTTGGCACAATACCTGCGCGCCTGCAACCTGG 1320
Db 1261 GTACCTGCAAGAAATTTAAACCATTTGGCACAATACCTGCGCGCCTGCAACCTGG 1320
QY 1321 CCAGTCCATCTTTTGGGAAGGGAATGTGCCCTTCCCTGCTTCCACTCGGTGGAGCGGTG 1380
Db 1321 CCAGTCCATCTTTTGGGAAGGGAATGTGCCCTTCCCTGCTTCCACTCGGTGGAGCGGTG 1380
QY 1381 AGGAGGCTTGGTCTCCGCTGGGAGAGTGACACGAGTCCGTCGTCGTCGTCGTCGGA 1440
Db 1381 AGGAGGCTTGGTCTCCGCTGGGAGAGTGACACGAGTCCGTCGTCGTCGTCGTCGGA 1440
QY 1441 CCAGCAGAGAGCGCGTCTCTGTGAGCTCACCAGCAACACCTGCTTGGGCGCTCGATCC 1500
Db 1441 CCAGCAGAGAGCGCGTCTCTGTGAGCTCACCAGCAACACCTGCTTGGGCGCTCGATCC 1500
QY 1501 AGACAGGGCTTGGAGTGTGAGCAAGTGTGACACCGCATCCGGCAGGACGCGGCTGGA 1560
Db 1501 AGACAGGGCTTGGAGTGTGAGCAAGTGTGACACCGCATCCGGCAGGACGCGGCTGGA 1560
QY 1561 GCACCTGGTCACTTGGTCTTCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1620
Db 1561 GCACCTGGTCACTTGGTCTTCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1620
QY 1621 TCCGCTCTGCAACTCCCGAGTGCCTCCAGATGGGGGCAAGAAATTCGAAAGGAGTGGCC 1680
Db 1621 TCCGCTCTGCAACTCCCGAGTGCCTCCAGATGGGGGCAAGAAATTCGAAAGGAGTGGCC 1680
QY 1681 GGGAGACCAAGCCTGCCAGGGCGCCCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1740
Db 1681 GGGAGACCAAGCCTGCCAGGGCGCCCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1740
QY 1741 CCCCGTGGTGGGCTGCACTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1800
Db 1741 CCCCGTGGTGGGCTGCACTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1800
QY 1801 GCAACAGCCCTGAGGCTCAGTACGAGGGAAGGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCG 1860
Db 1801 GCAACAGCCCTGAGGCTCAGTACGAGGGAAGGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCG 1860
QY 1861 AGATGTGCAACAGAGGAGCTGCCCGCTGGATGGCTGTTTATCCAAACCCCTGCTCCCGG 1920
Db 1861 AGATGTGCAACAGAGGAGCTGCCCGCTGGATGGCTGTTTATCCAAACCCCTGCTCCCGG 1920
QY 1921 GAGCCAGTGCAGAGCTTCCCGGATGGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1980
Db 1921 GAGCCAGTGCAGAGCTTCCCGGATGGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1980
QY 1981 TCTTGGCAATGGCACCCACTGTGAGGACCTGAGAGTGTGCCCTGCTGCCGACATCT 2040
Db 1981 TCTTGGCAATGGCACCCACTGTGAGGACCTGAGAGTGTGCCCTGCTGCCGACATCT 2040
QY 2041 GCTTCTCCACAGAGGAGTGCCTGCTGTCAACACTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2041 GCTTCTCCACAGAGGAGTGCCTGCTGTCAACACTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
QY 2101 CCGTCCCGCGGATACAGAGGAACACCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 2160
Db 2101 CCGTCCCGCGGATACAGAGGAACACCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 2160
QY 2161 CGGAAAGCAAGTGTGTGAGCGCCGCAACCCATGCAAGGACCAAGACACACAACTGCCACA 2220
Db 2161 CGGAAAGCAAGTGTGTGAGCGCCGCAACCCATGCAAGGACCAAGACACACAACTGCCACA 2220
QY 2221 AGCAGCGGAGTGCATCTACCTGGTCTGCTGAGGACCCCATGTCAGGAGCCCATGTCAGAGTGG 2280
Db 2221 AGCAGCGGAGTGCATCTACCTGGTCTGCTGAGGACCCCATGTCAGGAGCCCATGTCAGAGTGG 2280
QY 2281 AGACAGGCTACGCGGCGGACGCGCTCATCTGCGGGGAGGACTCGGACCTGGACGCTGCG 2340
Db 2281 AGACAGGCTACGCGGCGGACGCGCTCATCTGCGGGGAGGACTCGGACCTGGACGCTGCG 2340

[illegible]

| | | | |
|----|------|---|------|
| Db | 3421 | CCGGCGTGTCCCTCAAGTGGTGAAGTCCACACGGGGAGCGGCGAGCACCTTGAGGAACG | 3480 |
| Qy | 3481 | CGCTGTGGCACACGGGGAACACACGCCGGGCGCAGTGCAGCACTTATGGCACGACCCACGGA | 3540 |
| Db | 3481 | CGCTGTGGCACACGGGGAACACACGCCGGGCGCAGTGCAGCACTTATGGCACGACCCACGGA | 3540 |
| Qy | 3541 | ACATTGGCTGGAAGGACTACACGGCCCTATAGGTGGCCACCTGACTCACAGGCCCAAGACCG | 3600 |
| Db | 3541 | ACATTGGCTGGAAGGACTACACGGCCCTATAGGTGGCCACCTGACTCACAGGCCCAAGACCG | 3600 |
| Qy | 3601 | GCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACTCAGAGCCTATCT | 3660 |
| Db | 3601 | GCTACATCAGAGTCTTAGTGCATGAAGGAAAACAGGTCATGGCAGACTCAGAGCCTATCT | 3660 |
| Qy | 3661 | ATGACCAAACTCAGCTGGCGGGCGCTGGGTCTATTCTCTCTCTCTCAAGAATGGTCT | 3720 |
| Db | 3661 | ATGACCAAACTCAGCTGGCGGGCGCTGGGTCTATTCTCTCTCTCTCAAGAATGGTCT | 3720 |
| Qy | 3721 | ATTTCTCAGACCTCAAGTACGAATCAGAGATATTTAAACAAGATTGCTGCATTCCCG | 3780 |
| Db | 3721 | ATTTCTCAGACCTCAAGTACGAATCAGAGATATTTAAACAAGATTGCTGCATTCCCG | 3780 |
| Qy | 3781 | CAATGCCCTGTGCATGCCATGGTCCCTAGACACTCAGTTCATTTGGTTCCTTGGCGGTT | 3840 |
| Db | 3781 | CAATGCCCTGTGCATGCCATGGTCCCTAGACACTCAGTTCATTTGGTTCCTTGGCGGTT | 3840 |
| Qy | 3841 | CTCTCTCTACGACACTCCTGCTGCCCTTGACCTTAACCTCTGATGGTCTTCACTCTCTGC | 3900 |
| Db | 3841 | CTCTCTCTACGACACTCCTGCTGCCCTTGACCTTAACCTCTGATGGTCTTCACTCTCTGC | 3900 |
| Qy | 3901 | CAGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAATCAGAGATGAAC | 3960 |
| Db | 3901 | CAGCAACCCCAACCCCAAGTGCCTTCAGAGGATAAATATCAATGGAATCAGAGATGAAC | 3960 |
| Qy | 3961 | ATCTAACCCACTAGAGAAACACAGTTTGGTGATATATGAGACTTTATGTGGAGTGAAAT | 4020 |
| Db | 3961 | ATCTAACCCACTAGAGAAACACAGTTTGGTGATATATGAGACTTTATGTGGAGTGAAAT | 4020 |
| Qy | 4021 | TGGCGATGCCATTACATGCTTTTTCTGTTGTTTAAAAAAGTACAGTTTACATATAA | 4080 |
| Db | 4021 | TGGCGATGCCATTACATGCTTTTTCTGTTGTTTAAAAAAGTACAGTTTACATATAA | 4080 |
| Qy | 4081 | AATGTAATTACTTATTTATGTTATGTTATATGGAGTTCAAGGGAATACTGTGATAAGC | 4140 |
| Db | 4081 | AATGTAATTACTTATTTATGTTATATGGAGTTCAAGGGAATACTGTGATAAGC | 4140 |
| Qy | 4141 | CATTATGATAAATTAAGCATGAAAAATAATGCTGAACACTACTTTTGGTCTTAAAAAGTGTG | 4200 |
| Db | 4141 | CATTATGATAAATTAAGCATGAAAAATAATGCTGAACACTACTTTTGGTCTTAAAAAGTGTG | 4200 |
| Qy | 4201 | ACTATTCTTGAATTAGAGTTGCTCTACAAATGACACAAATCCCCTCAATTAATATAA | 4260 |
| Db | 4201 | ACTATTCTTGAATTAGAGTTGCTCTACAAATGACACAAATCCCCTCAATTAATATAA | 4260 |
| Qy | 4261 | ACAAGGTCGAATTCAAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTAAGAGACAACAGG | 4320 |
| Db | 4261 | ACAAGGTCGAATTCAAAATTTGAAGTAATGTTTTAGTAAGGAGAGATTAAGAGACAACAGG | 4320 |
| Qy | 4321 | CATAGCAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAAACAGTTACAAAA | 4380 |
| Db | 4321 | CATAGCAATGACATAAGCTACCGATTAACTAATCGGAACATGTAAAAACAGTTACAAAA | 4380 |
| Qy | 4381 | TAAACGAACCTCCTCTTGTTGCTTACAAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTT | 4440 |
| Db | 4381 | TAAACGAACCTCCTCTTGTTGCTTACAAATGAAAGCCCTCATGTGCAGTAGAGATGCAGTTT | 4440 |
| Qy | 4441 | CATCAAGAACAAACATCCTTGCAAATGGGTGTGACCGGTTCCAGATGTGGATTGGCA | 4500 |
| Db | 4441 | CATCAAGAACAAACATCCTTGCAAATGGGTGTGACCGGTTCCAGATGTGGATTGGCA | 4500 |
| Qy | 4501 | AAACCTCATTTAAGTAAAAAGGTTAGCAGAGCAAGTGCAGGTCCTTAGCTGCTGTTGTG | 4560 |

| | | | |
|----|------|--|------|
| Qy | 421 | ACTACATCCACCGGTGAACGCGAGATGACCTCAGCAAGATCACCAAGATCATATCGCGGAGA | 480 |
| Db | 421 | ACTACATCCACCGGTGAACGCGAGATGACCTCAGCAAGATCACCAAGATCATATCGCGGAGA | 480 |
| Qy | 481 | AGGAGGGCTTCTTCCTCAGCGGCCACGCTCAAGCAGGACGGCAAGTCCAGGGGCACGCTGT | 540 |
| Db | 481 | AGGAGGGCTTCTTCCTCAGCGGCCACGCTCAAGCAGGACGGCAAGTCCAGGGGCACGCTGT | 540 |
| Qy | 541 | TGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGACGTTGGAGATGGTCTCCAACGCCGCCG | 600 |
| Db | 541 | TGGCTCTGGAGGGCCCCGGTCTCTCCAGAGGACGTTGGAGATGGTCTCCAACGCCGCCG | 600 |
| Qy | 601 | CGACACGCTGGATCTACACTACTGATTTGAGCGGACCCGGCATGTGGTCTCTCCCTGGAGG | 660 |
| Db | 601 | CGACACGCTGGATCTACACTACTGATTTGAGCGGACCCGGCATGTGGTCTCTCCCTGGAGG | 660 |
| Qy | 661 | ACGTGGCCCTGGCTGACTCGCAGTGGAAAGACGTCACCGTCGACGTGGCTGGCCAGACCT | 720 |
| Db | 661 | ACGTGGCCCTGGCTGACTCGCAGTGGAAAGACGTCACCGTCGACGTGGCTGGCCAGACCT | 720 |
| Qy | 721 | ACAGCTTTGACAGTGGGCTCGCACTCATAGSACCAAGTTGCTCTGGACGAGCCCTTCTACG | 780 |
| Db | 721 | ACAGCTTTGACAGTGGGCTCGCACTCATAGSACCAAGTTGCTCTGGACGAGCCCTTCTACG | 780 |
| Qy | 781 | AGCACCTTCAGGCGGGAAGAAAGACCGGATGTAGTGGCCAAAGGCTCTGCCAGAGAGATC | 840 |
| Db | 781 | AGCACCTTCAGGCGGGAAGAAAGACCGGATGTAGTGGCCAAAGGCTCTGCCAGAGAGATC | 840 |
| Qy | 841 | ACTTCAGGGGTTTTCCTCAGAACGTCACACTAGTCTTTGAAAACCTCTCTGGAAGATATTC | 900 |
| Db | 841 | ACTTCAGGGGTTTTCCTCAGAACGTCACACTAGTCTTTGAAAACCTCTCTGGAAGATATTC | 900 |
| Qy | 901 | TAAGCAAGAAAGGTTGCCACGCAAGCCAGGAGCTGAGATCAACGCCATCATAGTCAGAACA | 960 |
| Db | 901 | TAAGCAAGAAAGGTTGCCACGCAAGCCAGGAGCTGAGATCAACGCCATCATAGTCAGAACA | 960 |
| Qy | 961 | CAGAGACGTTCGCGCTTGGTTCGCATGTCCACACCGAGTACGTGGGGCCCCAGCTCGGAGA | 1020 |
| Db | 961 | CAGAGACGTTCGCGCTTGGTTCGCATGTCCACACCGAGTACGTGGGGCCCCAGCTCGGAGA | 1020 |
| Qy | 1021 | GGAGGCCGAGGTTCGGAAACGCTCGTCGGAGAGCTGGGAACATGGTCCAGGAGCTCT | 1080 |
| Db | 1021 | GGAGGCCGAGGTTCGGAAACGCTCGTCGGAGAGCTGGGAACATGGTCCAGGAGCTCT | 1080 |
| Qy | 1081 | CGGGGCTCCACGTCCTCGTGAACACAGCTCAGCGGAAACCTCAAGAGAGTGTGCAATGATA | 1140 |
| Db | 1081 | CGGGGCTCCACGTCCTCGTGAACACAGCTCAGCGGAAACCTCAAGAGAGTGTGCAATGATA | 1140 |
| Qy | 1141 | ACAGTTTCTCTGGGAGCTCATTTGTTGGCCCTCTCTTAAGACAAGGAACATGTCAGCTTGCT | 1200 |
| Db | 1141 | ACAGTTTCTCTGGGAGCTCATTTGTTGGCCCTCTCTTAAGACAAGGAACATGTCAGCTTGCT | 1200 |
| Qy | 1201 | GGCAGGATGGCCGTTCTTTGGCGGAAATGAACCTGGTGGTGGACAGCTGCACACGCT | 1260 |
| Db | 1201 | GGCAGGATGGCCGTTCTTTGGCGGAAATGAACCTGGTGGTGGACAGCTGCACACGCT | 1260 |
| Qy | 1261 | GTACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACCTGCCCGCTTCAACCTCGG | 1320 |
| Db | 1261 | GTACCTGCAAGAAATTTAAACCATTTGGCCACCAATCACCTGCCCGCTTCAACCTCGG | 1320 |
| Qy | 1321 | CCAGTTCATCCTTTGTGGAGGCGAATGTGCGCTTCTGCTCCACTCGGTGGACGGTG | 1380 |
| Db | 1321 | CCAGTTCATCCTTTGTGGAGGCGAATGTGCGCTTCTGCTCCACTCGGTGGACGGTG | 1380 |
| Qy | 1381 | AGAGGGCTGCTCCGTCGGCAGAGTGACACCGCTGCTCCGTGACGTGTGGCTCTGGGA | 1440 |
| Db | 1381 | AGAGGGCTGCTCCGTCGGCAGAGTGACACCGCTGCTCCGTGACGTGTGGCTCTGGGA | 1440 |
| Qy | 1441 | CCAGCAGAGAGGCCGGTCTGTGACGTCACACGAAACACCTGCTGGGGCCCTCGATCC | 1500 |
| Db | 1441 | CCNAGAGAGAGGCCGGTCTGTGACGTCACACGAAACACCTGCTGGGGCCCTCGATCC | 1500 |
| Qy | 1501 | AGACACGGGCTTCAGTCTTGACAAAGTGTGACACCCCGATCCGGCAGAGACGGCGCTGGA | 1560 |

| | | | | |
|----|------|--|---|------|
| Db | 1501 | AGACACGGGCTTG | CAGTCTCTGAGCAAGTGTGACACCCGCACTCCGGCAGAGACGCGCGCTGGA | 1560 |
| QY | 1561 | GCCACTGGTACACCTTGGCTTTCATGCTCTGTCGACCTGTGGAGTTCGCAATATCAACACGA | 1620 | |
| Db | 1561 | GCCACTGGTACACCTTGGCTTTCATGCTCTGTCGACCTGTGGAGTTCGCAATATCAACACGA | 1620 | |
| QY | 1621 | TCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGGCAAGAATTGCAAGGGAGTGCC | 1680 | |
| Db | 1621 | TCCGTCTCTGCAACTCCCCAGTGCCCCAGATGGGGGGCAAGAATTGCAAGGGAGTGCC | 1680 | |
| QY | 1681 | GGGAGACAAAGCCTGCCAGGGGCCCCCATGCCCAATCGATGGCGCTGGAGCCCTGGT | 1740 | |
| Db | 1681 | GGGAGACAAAGCCTGCCAGGGGCCCCCATGCCCAATCGATGGCGCTGGAGCCCTGGT | 1740 | |
| QY | 1741 | CCCCGTGGTGGCGCTGCACCTGTCCACTGTGCCGTGGGATCCGGAGGCGCACCCGGGCT | 1800 | |
| Db | 1741 | CCCCGTGGTGGCGCTGCACCTGTCCACTGTGCCGTGGGATCCGGAGGCGCACCCGGGCT | 1800 | |
| QY | 1801 | GCAACAGCCCTGAGCCCTCAGTACGAGGGAAGSCCTGCCTGGGGATGTGCAGGAGCGTC | 1860 | |
| Db | 1801 | GCAACAGCCCTGAGCCCTCAGTACGAGGGAAGSCCTGCCTGGGGATGTGCAGGAGCGTC | 1860 | |
| QY | 1861 | AGATGTGCAACAGAGAGAGCTGCCCGTGGATGGCTGTTTATCAAACCCCTGCTTCCCGG | 1920 | |
| Db | 1861 | AGATGTGCAACAGAGAGAGCTGCCCGTGGATGGCTGTTTATCAAACCCCTGCTTCCCGG | 1920 | |
| QY | 1921 | GAGCCCACTGACAGAGCTTCCCAGATGGGTGCTGTGTCATGCGGCTTCGCCCTGGGCT | 1980 | |
| Db | 1921 | GAGCCCACTGACAGAGCTTCCCAGATGGGTGCTGTGTCATGCGGCTTCGCCCTGGGCT | 1980 | |
| QY | 1981 | TCCTTGGGCAATGGCACCCACTGTGAGGACCTGGACAGTGTGCCCTGGTCCCGACATCT | 2040 | |
| Db | 1981 | TCCTTGGGCAATGGCACCCACTGTGAGGACCTGGACAGTGTGCCCTGGTCCCGACATCT | 2040 | |
| QY | 2041 | GCTTCTCACAGCAAGGTGCCTCGTGTGTCAACACTCAGCCTGGCTTCCACTGCCTGC | 2100 | |
| Db | 2041 | GCTTCTCACAGCAAGGTGCCTCGTGTGTCAACACTCAGCCTGGCTTCCACTGCCTGC | 2100 | |
| QY | 2101 | CCTGCCGCCCGATACAGAGGAACACGCCGTGGGGTTCGGCTGGAAGCAGCCAGA | 2160 | |
| Db | 2101 | CCTGCCGCCCGATACAGAGGAACACGCCGTGGGGTTCGGCTGGAAGCAGCCAGA | 2160 | |
| QY | 2161 | CGGAAAGCAAGTGTGTGAGCCCGGAAAACCCATGCAAGGACAAAGACACAACTGCCACA | 2220 | |
| Db | 2161 | CGGAAAGCAAGTGTGTGAGCCCGGAAAACCCATGCAAGGACAAAGACACAACTGCCACA | 2220 | |
| QY | 2221 | AGCAGCGGGAGTGCATCTACTGGGTCACTTCAGCGACCCCATGTACAAGTGCAGTGCC | 2280 | |
| Db | 2221 | AGCAGCGGGAGTGCATCTACTGGGTCACTTCAGCGACCCCATGTACAAGTGCAGTGCC | 2280 | |
| QY | 2281 | AGCAGGCTACGCGGGCGAGGGCTCATCTGCGGGGAGCCTCGGACCTGGACGCTGGC | 2340 | |
| Db | 2281 | AGCAGGCTACGCGGGCGAGGGCTCATCTGCGGGGAGCCTCGGACCTGGACGCTGGC | 2340 | |
| QY | 2341 | CCAACTCAATCTGGTCTGCGCCACCAAGCCACCTACCACCTGCATCAAGGATAACTGCC | 2400 | |
| Db | 2341 | CCAACTCAATCTGGTCTGCGCCACCAAGCCACCTACCACCTGCATCAAGGATAACTGCC | 2400 | |
| QY | 2401 | CCCATCTGCCAAATCTTGGGCGAGGAGACTTTGACAAGGACGGGATGGCGATGCCCTGTG | 2460 | |
| Db | 2401 | CCCATCTGCCAAATCTTGGGCGAGGAGACTTTGACAAGGACGGGATGGCGATGCCCTGTG | 2460 | |
| QY | 2461 | ATGATGAGGATGACAATGACGCTGTGACCGATGAGAGGACAACTGCCAGTCTCTCTTCA | 2520 | |
| Db | 2461 | ATGATGAGGATGACAATGACGCTGTGACCGATGAGAGGACAACTGCCAGTCTCTCTTCA | 2520 | |
| QY | 2521 | ATCCCGCCAGGCTGACTATGACAAGGATGAGGTGGGGACCGCTGTGACAACCTGCCCTT | 2580 | |
| Db | 2521 | ATCCCGCCAGGCTGACTATGACAAGGATGAGGTGGGGACCGCTGTGACAACCTGCCCTT | 2580 | |
| QY | 2581 | ACGTGCACACCCCTGCCCAGATCGACACAGACAACAAATGGAGGGGTGACGCTGCTCCG | 2640 | |


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QY 4801 ATTTTAAATATGCTAGTAAACATATGTAGTATAATTTCTAGAAACAACATCTAATAA 4860
Db 4801 ATTTTAAATATGCTAGTAAACATATGTAGTATAATTTCTAGAAACAACATCTAATAA 4860
QY 4861 GTATATAATCCTGTGAAATATAGGCTTGATAATATATAGTTGTACGATGAAGCATGC 4920
Db 4861 GTATATAATCCTGTGAAATATAGGCTTGATAATATATAGTTGTACGATGAAGCATGC 4920
QY 4921 TAGAAGCTGTAAACAGATACATAGAGAAATATAGAGAGTTTATGATGAACCTTAATAATA 4980
Db 4921 TAGAAGCTGTAAACAGATACATAGAGAAATATAGAGAGTTTATGATGAACCTTAATAATA 4980
QY 4981 TAATGTTGCCAGCGATTTTAGTTCATATATTTGTTTACTGTTATCTATCTGCTGTATATGGA 5040
Db 4981 TAATGTTGCCAGCGATTTTAGTTCATATATTTGTTTACTGTTATCTATCTGCTGTATATGGA 5040
QY 5041 ATTCCTTTTAAATCAACCGCTGAAACGAATCAGCATTTAGTCTTTGCCAGGCACACCCCAAT 5100
Db 5041 ATTCCTTTTAAATCAACCGCTGAAACGAATCAGCATTTAGTCTTTGCCAGGCACACCCCAAT 5100
QY 5101 AATCAGTCATGTGTAATATGACAAAGTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 5160
Db 5101 AATCAGTCATGTGTAATATGACAAAGTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG 5160
QY 5161 TTTTTTCTTAAAGTTCATGATCTTTCTGCAGGAATATGCTCACTCATCCACTCCACAT 5220
Db 5161 TTTTTTCTTAAAGTTCATGATCTTTCTGCAGGAATATGCTCACTCATCCACTCCACAT 5220
QY 5221 AAGGGGTTTATAGTAAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 5280
Db 5221 AAGGGGTTTATAGTAAGAAAGTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 5280
QY 5281 CCTTCTGTTAAATAGTATCATCTTCTATGCCAAACAGGAACGATCCATAACTTTTATGTC 5340
Db 5281 CCTTCTGTTAAATAGTATCATCTTCTATGCCAAACAGGAACGATCCATAACTTTTATGTC 5340
QY 5341 TTAATGTACACATGTCATTTTATGATAAATTAATTTTCTGTTTCTGTTGAGTTGATCGT 5400
Db 5341 TTAATGTACACATGTCATTTTATGATAAATTAATTTTCTGTTTCTGTTGAGTTGATCGT 5400
QY 5401 TGTGTTGTTTGTGTCACACTTTTACTTTTTTTCGCTGTGGAGCTGATTTCCGAGACAACG 5460
Db 5401 TGTGTTGTTTGTGTCACACTTTTACTTTTTTTCGCTGTGGAGCTGATTTCCGAGACAACG 5460
QY 5461 AAGGGTTGGGATCTTCAATTAATGTAGCGACTGTCAACAGCGTGCAGGTTTCTGTTTC 5520
Db 5461 AAGGGTTGGGATCTTCAATTAATGTAGCGACTGTCAACAGCGTGCAGGTTTCTGTTTC 5520
QY 5521 TGTGTTGTTGGGTCAACCGTACAATGTTGTGGGAATGACGATGATGTGAATATTTAGAAAT 5580
Db 5521 TGTGTTGTTGGGTCAACCGTACAATGTTGTGGGAATGACGATGATGTGAATATTTAGAAAT 5580
QY 5581 GTACCATATTTTGTGTAATTTATTTATGTTTTTCTTAAACAAATTTATCGTATAGTTTCAT 5640
Db 5581 GTACCATATTTTGTGTAATTTATTTATGTTTTTCTTAAACAAATTTATCGTATAGTTTCAT 5640
QY 5641 GAAACGTCATGTGTTTTGCCAAAGACGTAAATATTTATTTATGTTGTTACATGGTCAAA 5700
Db 5641 GAAACGTCATGTGTTTTGCCAAAGACGTAAATATTTATTTATGTTGTTACATGGTCAAA 5700
QY 5701 ATTTTACCACCTGAAACCCCTGCATCTAGTAAACCTCATTTTAAAGNTTAAACAACAGGA 5760
Db 5701 ATTTTACCACCTGAAACCCCTGCATCTAGTAAACCTCATTTTAAAGNTTAAACAACAGGA 5760
QY 5761 AATAAATTTGAAAAAGGTTTTTCT 5784
Db 5761 AATAAATTTGAAAAAGGTTTTTCT 5784
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RESULT 3

US-09-925-301-189

: Sequence 189, Application US/09925301

: Patent No. US20020052308A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
; LENGTH: 3787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (155)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-189
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Query Match          63.7%; Score 3683.4; DB 10; Length 3787;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3722; Conservative 5; Mismatches 7; Indels 8; Gaps 3;
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QY 2051 CAGCAAGTGCCTCGCTGTGTCAACACTCAGCCCTGGCTTCCACTGCTGCTGCCGCC 2110
Db 34 CAGCAAGTGCCTCGCTGTGTCAACACTCAGCCCTGGCTTCCACTGCTGCTGCCGCC 93
QY 2111 CCGATACAGAGGAACCAAGCCGCTCGGGTGGCTGGAAGCAGCCAGAGGAAAGCA 2170
Db 94 CCGATACAGAGGAACCAAGCCGCTCGGGTGGCTGGAAGCAGCCAGAGGAAAGCA 153
QY 2171 AGTGTGTAGCCCGAAACCCCATGCAAGGACAAGACACAACTGCCACAGACGCGGA 2230
Db 154 ANTGTGTAGCCCGAAACCCCATGCAAGGACAAGACACAACTGCCACAGACGCGGA 213
QY 2231 GTGCATCTACCTGGTGTCACTTCAGCGACCCCATGTACAAAGTGCAGTSCCAGACGGCTA 2290
Db 214 GTGCATCTACCTGGTGTCACTTCAGCGACCCCATGTACAAAGTGCAGTSCCAGACGGCTA 273
QY 2291 CGCGGCGACGGGCTCATCTCGGGGAGGACTCGGACCTGGACGGCTGGCCCAACCTCAA 2350
Db 274 CGCGGCGACGGGCTCATCTCGGGGAGGACTCGGACCTGGACGGCTGGCCCAACCTCAA 333
QY 2351 TCTGGTCTGGCCACCAACGCCACTTACCATGTCAAGGATTAACCTGCCCCCATCTGCC 2410
Db 334 TCTGGTCTGGCCACCAACGCCACTTACCATGTCAAGGATTAACCTGCCCCCATCTGCC 393
QY 2411 AAATTCCTGGGACGAGAACTTTTGACAGGAGGGATTGGCGATGCTGTGATGATGAGA 2470
Db 394 AAATTCCTGGGACGAGAACTTTTGACAGGAGGGATTGGCGATGCTGTGATGATGAGA 453
QY 2471 TGACAATGACGGTGTGACCGCATGAGAGGACAACCTGCCAGCTCCTCTTCAATCCCGCCA 2530
Db 454 TGACAATGACGGTGTGACCGCATGAGAGGACAACCTGCCAGCTCCTCTTCAATCCCGCCA 513
QY 2531 GGCTGACTATGACAAGGATGAGTTGGGACCGGTGTGACAACCTGCCCTTACGTGCACAA 2590
Db 514 GGCTGACTATGACAAGGATGAGTTGGGACCGGTGTGACAACCTGCCCTTACGTGCACAA 573
QY 2591 CCCTGCCAGATCGACACAGACAACTGGAGAGGGTGACGCCCTGCTCCGTGGACATGA 2650
Db 574 CCCTGCCAGATCGACACAGACAACTGGAGAGGGTGACGCCCTGCTCCGTGGACATGA 633
QY 2651 TGGGACGATGCTTCAATGAACGAGACAATTTGTCCTTACCTTACAACTGACACAG 2710
Db 634 TGGGACGATGCTTCAATGAACGAGACAATTTGTCCTTACCTTACAACTGACACAG 693
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Db 781 CGAGTACGTGGGCCCCAGCTCAGAGAGGAGGCCGAGGTGTGGAAACGCTCGTGCAGGA 840
QY 1055 GCTGGGAAACATAGTTCAGGAGCTCTCGGGGCTTCCACGCTCCTCGTGAACACAGCTCAGCGA 1114
Db 841 GCTGGGAAACATAGTTCAGGAGCTCTCGGGGCTTCCACGCTCCTCGTGAACACAGCCACGGA 900
QY 1115 GAACCTCAAGAGAGTGTCAATGATTAACCAAGTTTCTCTGGGAGCTCATTTGGTGGCCCTCC 1174
Db 901 GAACCTCAAGAGAGTGTCAATGATTAACCAAGTTTCTCTGGGAGCTCATTTGGTGGCCCTCC 960
QY 1175 TAAGACAAGGAACATCTCAGCTTGCTGGCAGGATGCCGCTTCTTTGCGGAAATGAAC 1234
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QY 1235 GTGGGTGGTGGAGAGTGCACACACGCTGTACCTGCAAGAAATTTAAACCATTTTGGCCACCA 1294
Db 1021 GTGGGTGGTGGAGAGTGCACACACGCTGTACCTGCAAGAAATTTAAACCATTTTGGCCACCA 1080
QY 1295 AATCACCCTGCCCTGCAACCTGGCCAGTCCATCCTTTGTGGAGGGGAATGTGCC 1354
Db 1081 AATCACCCTGCCCTGCAACCTGGCCAGTCCATCCTTTGTGGAGGGGAATGTGCC 1140
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Db 1141 TTCTGCCCTCCACTCGTGGAGCGGTGAGGAGGCTGGTCTCGTGGGACAGTGGACCCA 1200
QY 1415 GTGCTCCGTGACGTGTGGCTTGGACCCAGCAGAGAGCCGCTCCTGTGACGTCAACCA 1474
Db 1201 GTGCTCCGTGACGTGTGGCTTGGACCCAGCAGAGAGCCGCTCCTGTGACGTCAACCA 1260
QY 1475 CAACACCTGCTTGGGCCCTCATCCAGACAGCGGCTTGCACTGTGAGCAAGTGTGACAC 1534
Db 1261 CAACACCTGCTTGGGCCCTCATCCAGACAGCGGCTTGCACTGTGAGCAAGTGTGACAC 1320
QY 1535 CGGCATCCGGCAGGAGCGGCTGGAGCCACTGGTCACTTGGTCTTCACTGTCTGTGAC 1594
Db 1321 CGGCATCCGGCAGGAGCGGCTGGAGCCACTGGTCACTTGGTCTTCACTGTCTGTGAC 1380
QY 1595 CTGTGGAGTTGGCAATATACACAGCATCGTCTCTGCAACTCCCACTGCCCCAGATGGG 1654
Db 1381 CTGTGGAGTTGGCAATATACACAGCATCGTCTCTGCAACTCCCACTGCCCCAGATGGG 1440
QY 1655 GGGCAAGAAATCCAAAGGAGTGGCCGGAGACCAAGCCTGCCAGGGGCCCATGGCC 1714
Db 1441 GGGCAAGAAATCCAAAGGAGTGGCCGGAGACCAAGCCTGCCAGGGGCCCATGGCC 1500
QY 1715 AATCATGGCCCTGGAGCCCTGGTCCCGTGGTCCGGCTGCACTGTCACTGTGCGCG 1774
Db 1501 AATCATGGCCCTGGAGCCCTGGTCCCGTGGTCCGGCTGCACTGTCACTGTGCGCG 1560
QY 1775 TGGGATCCGGGAGCGACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGAAGGC 1834
Db 1561 TGGGATCCGGGAGCGACCCGGGTCTGCAACAGCCCTGAGCCTCAGTACGGAGGGAAGGC 1620
QY 1835 CTGCGTGGGGATGTGCAGGAGCGTCAAGTGTGCACACAGAGAGGAGCTGCCCGTGGATGG 1894
Db 1621 CTGCGTGGGGATGTGCAGGAGCGTCAAGTGTGCACACAGAGAGGAGCTGCCCGTGGATGG 1680
QY 1895 CTGTTTATCCAAACCCTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTG 1954
Db 1681 CTGTTTATCCAAACCCTGCTTCCCGGAGCCAGTGCAGCAGCTTCCCGATGGGTCTCTG 1740
QY 1955 GTCATCGGGCTTCTGCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGA 2014
Db 1741 GTCATCGGGCTTCTGCCCTGTGGGCTTCTTGGGCAATGGCACCCACTGTGAGGACCTGGA 1800
QY 2015 GAGTGTGCCCTGTGCCGACATCTGCTTCCACACAGCAGAGTGCCTCGCTGTGTCAA 2074
Db 1801 GAGTGTGCCCTGTGCCGACATCTGCTTCTCCACACAGCAGAGTGCCTCGCTGTGTCAA 1860
QY 2075 CACTCAGGCTGGCTTCCACTGCTGCCCTGCCCGCCCGATACAGAGGGAACAGCCCGT 2134
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Db 1861 CACTCAGGCTGGTTCCACTGCTGCCCTGCCCGCCCGATACAGAGGGAACAGCCCGT 1920
QY 2135 CGGGGTGGCCCTGGAAGCAGCCAAAGCAGGAAAGAGTGTGTAGCCCGGAAACCCATG 2194
Db 1921 CGGGGTGGCCCTGGAAGCAGCCAAAGCAGGAAAGAGTGTGTAGCCCGGAAACCCATG 1980
QY 2195 CAAGGACAAAGACACAACTGCCAACAGCACGCGGAGTGCATCTACCTGGGCACCTTCAG 2254
Db 1981 CAAGGACAAAGACACAACTGCCAACAGCACGCGGAGTGCATCTACCTGGGCACCTTCAG 2040
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Db 2041 GCACCCCATGTAAAGTGGAGTGGCAGAGGCTACGCGGGCGAGGGCTCATCTGCCG 2100
QY 2315 GGAGGACTCGGACCTGGACGGCTGGCCAACTCAATCTGTCTGCGCCACCAAGCCAC 2374
Db 2101 GGAGGACTCGGACCTGGAGGGCTGGCCAACTCAATCTGTCTGCGCCACCAAGCCAC 2160
QY 2375 CTACCACTGCATCAAGGATACTGCCCCCATCTGCCAAATCTTGGCGAGGAAGACTTTGA 2434
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QY 2495 GAAGGACAACTGCCAGCTCCTCTTCAATCCCGCCGAGGTGACTATGACAAGGATGAGT 2554
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QY 2675 AGACAAATGTCCCTACGTCTACAACACTGACAGAGGACACGGATGTGACGGTGGG 2734
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QY 2735 GGATCAGTGTGACAACTGCCCTTGTGCACAACTTGCACAGACCGAGTGGGCAATGA 2794
Db 2521 GGATCAGTGTGACAACTGCCCTTGTGCACAACTTGCACAGACCGAGTGGGCAATGA 2580
QY 2795 CCTTCTTGGGACCACTGTGACAACTGAGGACATAGATGACGACGCGCACCAACAA 2854
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QY 2855 CCAGGACAACTGCCCTACATCTCCAACGCCAACCAAGCTGACCATGACAGAGCGGCA 2914
Db 2641 CCAGGACAACTGCCCTACATCTCCAACGCCAACCAAGCTGACCATGACAGAGCGGCA 2700
QY 2915 GGGCACCGCTGTGACCTGTGATGACAACTGCGGTGCCCGATGACAGGGGCAACTG 2974
Db 2701 GGGCACCGCTGTGACCTGTGATGACAACTGCGGTGCCCGATGACAGGGGCAACTG 2760
QY 2975 CGGGTCTGTGTTCAACCCAGACAGGAGCTTGGACGGTGTGACCGGGTGTATTTG 3034
Db 2761 CGGGTCTGTGTTCAACCCAGACAGGAGACTTGGACGGTGTGACCGGGTGTATTTG 2820
QY 3035 TAAAGATGATTTGACAAATGACAACTCCAGATATTGATGTGTGTCTGCTGAAACAA 3094
Db 2821 TAAAGATGATTTGACAAATGACAACTCCAGATATTGATGTGTGTCTGCTGAAACAA 2880
QY 3095 TGCCATCAGTGAAGACAGACTTCAGAACTTCAGATGTGTCCCTTGGATCCCAAGGGAC 3154
Db 2881 TGCCATCAGTGAAGACAGACTTCAGAACTTCAGATGTGTCCCTTGGATCCCAAGGGAC 2940
QY 3155 CACCCAAATTTGATCCCAACTGGTTCATTCGCCATCAAGGCAAGGAGCTGGTTTCACAGC 3214
Db 2941 CACCCAAATTTGATCCCAACTGGTTCATTCGCCATCAAGGCAAGGAGCTGGTTTCACAGC 3000

| | | | |
|----|------|---|------|
| Qy | 3215 | CAACTCGGACCCGGGCATCGCTGTAGGTTTTGACGAGTTTGGTGCTGTGGACTTCAGTGG | 3274 |
| Db | 3001 | CAACTCGGACCCGGGCATCGCTGTAGGTTTTGACGAGTTTGGTGCTGTGGACTTCAGTGG | 3060 |
| Qy | 3275 | CACATTCTAGTAAACACATGACCGGAGACGACACTATGCTGGCTTCGCTTTGGTTACCA | 3334 |
| Db | 3061 | CACATTCTAGTAAACACATGACCGGAGACGACACTATGCCGGCTTCGCTTTGGTTACCA | 3120 |
| Qy | 3335 | GTCAAGCAGCCGCTCTATGTGGTGTATGTGGAAGCAGGTGACGACAGCTACTGGGAGGA | 3394 |
| Db | 3121 | GTCAAGCAGCCGCTCTATGTGGTGTATGTGGAAGCAGGTGACGACAGCTACTGGGAGGA | 3180 |
| Qy | 3395 | CCAGCCACGCGGGCCTATGGTACTCCGGCGTCTCCCTCAAGGTGTGAACTCCACCAC | 3454 |
| Db | 3181 | CCAGCCACGCGGGCCTATGGTACTCCGGCGTCTCCCTCAAGGTGTGAACTCCACCAC | 3240 |
| Qy | 3455 | GGGGAGGGGAGCAGCACTCAGGAAACGCGCTGTGGCACACGCGGGGAAACAGCCGGGGCAGGT | 3514 |
| Db | 3241 | GGGGAGGGGAGCAGCACTCAGGAAACGCGCTGTGGCACACGCGGGGAAACAGCCGGGGCAGGT | 3300 |
| Qy | 3515 | GCGAACCTTATGGCAGCACCCAGGAACAATTGGCTGGAAGGACTACACGGCTTATAGGTG | 3574 |
| Db | 3301 | GCGAACCTTATGGCAGCACCCAGGAAACAATTGGCTGGAAGGACTACACGGCTTATAGGTG | 3360 |
| Qy | 3575 | GCACCTGACTACAGGCCCAAGACCGGCTACATCAGAGTCTTAGTGATGAAGGAAAACA | 3634 |
| Db | 3361 | GCACCTGACTACAGGCCCAAGACCGGCTACATCAGAGTCTTAGTGATGAAGGAAAACA | 3420 |
| Qy | 3635 | GGTCATGGCAGACTCAGGACCTATCTATGACCAACCTTACGCTGGCGGGCGGCTGGGTCT | 3694 |
| Db | 3421 | GGTCATGGCAGACTCAGGACCTATCTATGACCAACCTTACGCTGGCGGGCGGCTGGGTCT | 3480 |
| Qy | 3695 | ATTGTGCTTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATCGAGAGTAT | 3754 |
| Db | 3481 | ATTGTGCTTCTCTCAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATCGAGAGTAT | 3540 |
| Qy | 3755 | TTAAACAAGATTTGCTGCATTTTCGGGCATGGCCCTGTGCATGCCATGGTCCCTAGA | 3810 |
| Db | 3541 | TTAAACAAGATTTGCTGCATTTTCGGGCATGGCCCTGTGCATGCCATGGTCCCTAGA | 3596 |

RESULT 5

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US-09-880-107-3701
; Sequence 3701, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3701
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 x14787
US-09-880-107-3701

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Query Match 26.8%; Score 1550.4; DB 10; Length 5722;
Best Local Similarity 65.9%; Pred. NO. 0;
Matches 2326; Conservative 0; Mismatches 1171; Indels 33; Gaps 4;

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| Qy | 252 | CTGTCCTCTGGCTCTGTGGGTGGCCCGCAGCAGCTGTGTACAGGACAAAGAC | 311 |
| Db | 139 | CTGTTTCTGTATGATGTGTGTGCGCAACCAACCCGATCTCCAGAGTCTGTGGCGGAGACA | --AC 195 |
| Qy | 312 | ACGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGCACTATGGCGCCAAAGCAG | 371 |
| Db | 196 | AGCGTGTTCGACATCTTGAACATCACGGGGCGCCCGCAAGGGTCTGTGGCGCCGCACTG | 255 |
| Qy | 372 | TTCCCGCGGGCCGACACCCCGCGCTTACCGCTTCGTGCGCTTTTGACTTACATCCCA | 431 |
| Db | 256 | GTGAAGGCCCGCAGACCTTCCAGCCGAGCTTTCGGCATCGAGGATGCCAACCTGATCCCC | 315 |
| Qy | 432 | CCGCTGAACCGAGATGACCTCAGCAAGATCACCAAGATCATCGCGGAGAAGGAGGGCTTC | 491 |
| Db | 316 | CCTGTGCTGATGACAAAGTTTCCAAGACCTCGTGTGATGCTGTGTGCGGCAAGAAAGGTTTC | 375 |
| Qy | 492 | TTCCCTACGCGCCGACGCTCAGCAGGACGCGCAGTCCAGGGGCAAGCTGTTGGCTCTGGAG | 551 |
| Db | 376 | CTCCTCTTGCGATCCCTTGAGGCGAGATGAAGAGACCCGGGGCAGCTGCTGGCCCTGGAG | 433 |
| Qy | 552 | GGCCCCCGGTCTCTCCAGAGGCGAGTTTCGAGATCGTCTCCAACGGCGCCCGGACACGCTG | 611 |
| Db | 436 | CGGAAGACCACTCTGCCAGGTCTTCAGGTGGTGTCCAATGGCAAGCGGGCACCTG | 495 |
| Qy | 612 | GATCTCACCCTACTGGATTGACGGCAACCCGGCATGTGGTCTCCCTCGAGAGAGTCCGGCTG | 671 |
| Db | 496 | GACCTCAGCTGACCGTCCAAGAAAGCAGCAGTGGTGTCTGTGGAAGAAGCTCTCCTG | 555 |
| Qy | 672 | GCTCAGCTCGCAGTGAAGAAGCTTACCGTTCAGGTGGTGGCGAGACCTACAGTTCGAC | 731 |
| Db | 556 | GCAACCGGCGAGTGAAGAGCATCACCCCTGTTGTGACGAAGAAGAGGGGCCCGAGTGTAC | 615 |
| Qy | 732 | GTGGCTTCGCACTCATAGGACAGTTCGTCTGGAGCGCCCTTCTACGAGCACCTGCAG | 791 |
| Db | 616 | ATCAGCTGTGAAGAATGAGAAATGCTGAGTTGGAGTCCCCATCCAAGCGTCTTCACC | 675 |
| Qy | 792 | GCAGAAAGAGCGCGGATGTACGTGGCCAAAGGCTC-----TGCCAGAGAGTCACTTC | 845 |
| Db | 676 | AGAGACCTGGCCAGCATCGCCAGACTCCGCGATCGCAAGAGGGGGGTCAATGACAATTC | 735 |
| Qy | 846 | AGGGTTTTCCTTCAGAACGTCCACCTAGTGTGTTGAAACTCTGTGGAAGATATCTAAGC | 905 |
| Db | 736 | CAGGGGTGTGCAGAAATGTGAGGTTGTCTTTGGAACACACACCGAAGAGATCCTCAG | 795 |
| Qy | 906 | AAGAAGGTTTCCAGCAAGGCCAGGAGCTGAGATCAACGCCATCAGTGTGAGAACAACAG | 965 |
| Db | 796 | AACAAGGCTGC-----TCCAGCTTACCAGTGTCTCTCTCACCTGTGACAAACAGTG | 849 |
| Qy | 966 | ACGTGCGCCTGGTCCGATGTCAACCCGAGTAGTGTGGGCCCCAGCTCGGAGAGGAGG | 1025 |
| Db | 850 | GTGAATGTTTCCAGCCCTGCCATCCGCACTAACTACATTTGGCCCAAGACAAGGACTTG | 909 |
| Qy | 1026 | CCGAGGTGTGCGAACGCTCGTCGAGGAGCTGTGGGAACATGGTTCAGAGGCTCTCGGGG | 1085 |
| Db | 910 | CAAGCCATCTGCGGCACTCTCTGTGATGAGCTGTCCAGCATGGTCTGGAAGTCAAGGGC | 969 |
| Qy | 1086 | CTCCAGCTCTCTGTGAACCAAGCTCAGCGAGAACCTCAACAGAGTGTGCGAATGATAACAG | 1145 |
| Db | 970 | CTGGCGCAACATTTGTGACCAGCTGTGAGGACAGCATCCGCAAGTACTGTGAAGAGACAA | 1029 |
| Qy | 1146 | TTTCTCTGGGAGCTCATTTGGTGCCCTCTCTTAAGACAAGGAACATGTCAAGTTGTGGCAG | 1205 |
| Db | 1030 | GAGTTGGCCAATGAGCTGAGGGCGGCTC-----CCCTATGCTATCAC | 1071 |
| Qy | 1206 | GATGGCCGGTTCTTTGGGGAATAAGAACGTGGGTGGTGAGCAGCTGGCACACGTTGACC | 1265 |
| Db | 1072 | AACGGAGTTCAGTACAGAAATAACAGAGGAATGGAAGTGTGTATGATGCTGAGTGTGCAC | 1131 |
| Qy | 1266 | TGCAAGAAATTTAAACCATTTCCCAACAAATCACTGCCGCCCTGCACACCTGCCCACT | 1325 |
| Db | 1132 | TGTCAGAACTCAGTTACCATCTGCAAAAAGGTGTCTCTGCCCAATCATGCCCTGTCTCCAAT | 1191 |
| Qy | 1326 | CCATCTCTTGTGGAAGCGCAATGCTGCCCTCTCTGTGCTCCATCTCGGTGGAGCGGTGAGAG | 1385 |

Db 1192 GCACAGTTCTGTAGTGGAGAAATGCTGCTCGCTGTGGCCACGCACTCTCGGGACGAT 1251
QY 1386 GGTGTGTCCTCGGTGGGACAGAGTGGACCCAGTGTCTCGTGTGACGTGTGGCTCTGGGACCCAG 1445
Db 1252 GGTGTGTCCTCATGTGTCCAGTGGACCTCTCTGTCTACGAGCTGTGGCAATGGAATTCAG 1311
QY 1446 CAGAGAGGGCGGTCTCTGTGTACGTACCCAGCACAACACTGTGTGGGGCCCTTCGATCCAGACA 1505
Db 1312 CAGCGCGCGCGTCTCTGCGATAGCCTCAACAACCGATGTGAGGGCTCTCTCGGTCCAGACA 1371
QY 1506 CGGGCTTGCAGTCTGAGCAAGTGTACACCCGATCCGCGCAGCAGCGCGCGTGGAGCCAC 1565
Db 1372 CGGACTGCCAATTCAGAGAGTGTGACAAAGATTTAAACAGAGTGTGGCTGGAGCCAC 1431
QY 1566 TGGTCACTTGGTCTCTGTGACCTGTGGAGTTGGCAATATCACAGCATCCGT 1625
Db 1432 TGGTCCCCGTGTCTCTGTGTGTGACATGTGTGTGTGATCATCAAGGATCCGG 1491
QY 1626 CTCTGCACTCCCGAGTGCCTCAGATGGGGGGCAAGATTTGAAAGGGAGTGGCGGGAG 1685
Db 1492 CTCTGCACTCTCCAGCCCCCAGATGAATGGGAAACCTGTGAAAGGCAAGCGGGAG 1551
QY 1686 ACCAAGCTTGCAGGGCGCCCATGSCCAATCGATGGCGCTGGAGCCCTGGTCCCG 1745
Db 1552 ACCAAGCTTGCAGAAAGACGCTGCCCCATCAATGGAGGCTGGGGTCTTGGTCAACA 1611
QY 1746 TGGTGGCTGTCACTGTCACTGTGCGGTGGGATCCGGGAGCGCACCGGTCTGCAAC 1805
Db 1612 TGGGACATCTGTCTGTCACCTGTGGAGGAGGGTACAAACGTAGTCTCTGCAAC 1671
QY 1806 AGCCGTGACCTTCAGTACGGAGGGAAGGCTCGCTGGGGGATGTGAGAGGCGTCAGATG 1865
Db 1672 AAACCGCACCCCGATTTGGAGGCAAGGACTGCGTTGTGTGATGAACAAAGAACCAACGATC 1731
QY 1866 TGCAACAAGAGGAGTGCCTCGTGTGATGGCTGTATTCACAAACCCCTGCTCCGGGAGCC 1925
Db 1732 TGCAACAAGAGGAGTGCCTCAATGTATGGATGCCTGTCCAATGCCCTGTCCGGCGTG 1791
QY 1926 CAGTGCAGAGCTTCCCCGATGGTCTCTGTGTCATCGGGCTTCTGCCCTGTGGGCTCTTG 1985
Db 1792 AAGTGTACTAGTACCTGATGGCAGCTGGAATGTGGTGTCTGCCCTGTGTACAGT 1851
QY 1986 GCAATGGCACCCACTGTGAGACCTGTGACGAGTGTGCCCTGTGCCCGACATCTGCTTC 2045
Db 1852 GGAATGGCATCCAGTGCACAGATTTGATGAGTGCAGAAAGTGCCTGATGCCCTGCTTC 1911
QY 2046 TCCACACAGAGTGCCTCGCTGTGTCAACACTCAAGCTGAGCTTCCACTGCTGCCCTGC 2105
Db 1912 AACCAATGGAGAGCCGGTGTGAGACACGAGACCCCGGTACAACTGCTGCCCTGC 1971
QY 2106 CCGCCCCGATACAGAGGNAACCCCGTCCGGGTGCGGCTTGGAGCAGCCAGACGGAA 2165
Db 1972 CCCCCAGCTTCAACCGCTTCACAGCCCTTCGCGCCAGGTTGCGAATGTCACACGCCAAC 2031
QY 2166 AAGCAAGTGTGAGCCCGGAACCCATGCAAGGACAGACACAACTGCCACAAAGC 2225
Db 2032 AAACAGGTGTGAAGCCCCGTAAACCCCTGCACGGATGGGACCCACGACTGCACAAAGAAC 2091
QY 2226 GGGGAGTGCATCTACCTGGGTCACTTCAGCGACCCCATGTACAAGTGGAGTGCCAGACA 2285
Db 2092 GCCAAGTGCACACTCTGGGCCACATATAGCGACCCCATGTACCGCTGGAGTGCAGGCT 2151
QY 2286 GGTACGGGGGACGGGTCTATCTCGGGGAGGACTCGGACCTGGAGGGTGGCCCCAAC 2345
Db 2152 GGTACGGTGGCAATGGCATCTCTCGGGGAGGACACAGACCTTGATGGCTGGCCCAAT 2211
QY 2346 CTCATCTGCTTGGCCGACCAACCCACTTACCACTGCATCAAGGATAACTGGCCCCAT 2405
Db 2212 GAGAACCTGGTGTGGTGGCCCAATCGCACTTACCACCTGCACAAAGGATAATTTGCCCCAAC 2271
QY 2406 CTGCGCAAAATTCGGGACAGAGACTTTCACAGGAGCGGATTTGGCGATGCCCTGTGATGAT 2465

Db 2272 CTTCCAACTCAGGCGAGGAAGACTATGACAAGGATGGAATTTGGTGATGCCCTGTGATGAT 2331
QY 2466 GAGGATGACAATGACGGTGTGACCGATGAGAAGGACAACTGCGAGCTCTCTTCAATCC 2525
Db 2332 GAGGATGACAATGATAAATTTCCAGATGACAGGACAACTGTCCATTTCCATTACAAACCA 2391
QY 2526 CCGCAGGCTGACTATGACAAGGATGAGGTTGGGGACCGCTGTGACAACCTTACGTG 2585
Db 2392 GCTAGTATGACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACCTGTCCCTACAAC 2451
QY 2586 CACAACCTTGCACATGACACAGACAAATGAGAGGGTGTGAGCGCTGCTCCGTGGAC 2645
Db 2452 CACAACCCAGATCAGGACAGACACAAATGGGAAGGAGACCGCTGTGCTGCAGAC 2511
QY 2646 ATTGATGGGACGATGTCTTCAATGAACGAGACAAATTTGCTCCCTAGCTTACAACTGAC 2705
Db 2512 ATTGATGGAGACGGTATCCTCAATGAACGGGACAACTGCCAGTACGCTTACAATGTGGAC 2571
QY 2706 CAGAGGACACGAGTGGTGCCTGTGGGGATCTACTGTGACAACCTGCCCTGTGTCAC 2765
Db 2572 CAGAGAGACACTGATGTGATGGGTGGAGATCAGTGTGACAAATTTGCCCTTGGAAAC 2631
QY 2766 AACCTGACACGACCGTGGACAATGACCTTGTGGGACCACTGTGACAACACGAG 2825
Db 2632 AATCGGATCAGCTGAGCTGACTCAGACCCGATTTGGAGATACCTGTGACAACAACTAG 2691
QY 2826 GACATAGATGACAGGGCCACCAACACGAGCAACTGCCCTTACATCTCCAACGCC 2885
Db 2692 GATATTGATGAAGTGGCCACCAACAACTCTGGACAACCTGTCCCTATGTGCCAATGCC 2751
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Db 2752 AACAGGCTGACCATGACAAAGATGGCAAGGAGATGCTGTGACCACTGATGACAAAC 2811
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QY 3006 TTGACGCTGATGAGCGGGTGTATTTGTAAGATGATTTTGACAAATGACAACATCCCA 3065
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Db 3052 CATCAGGTAAAGAACTCGTCCAGACTGTCACTGTGATCTCTGGACTCGCTGTAGTTAT 3111
QY 3246 GACGAGTTTGGTCTGTGAGCTTCACTGAGTGCACATTTCTAGTAAACACTGACCGGACGAC 3305
Db 3112 GATGAGTTAATGTGTGTGAGCTTCACTGAGTGCACCTTCTTATCAACACCGAAAGGACGAT 3171
QY 3306 GACTATGCTGGCTTCTGTTTACCAGTCAACGACGCGCTTCTATGTGTGTGATGTGG 3365
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QY 3366 AAGCAGGTGACGACGACCTACTTGGGAGGACCAAGCCAGCGGGCCCTATGGCTACTCCGCG 3425
Db 3232 AAGCAAGTCAACCCAGTCTCTACTTGGGACACCAACCCACAGAGGCTCAGGATACTCGGCG 3291
QY 3426 GTGTCCTCAAGGTGCTGAATCTCACAGGGGAGCGGAGCAGCTTGAAGAACCGGTG 3485
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Db 3352 TGGCACACAGGAACACCCCTGGCCAGGTGGCCACCTGTGGCATGACCTCGTCACATA 3411

1610 ACCAAGCCCTGCAAGAAAGACGCTGCCCCATCAATGGAGGCTGGGGTCTTGGTCAACCA 1669
1746 TGGTCGGCTGCACTGTCACCTGTGCCGTGGGATCCGGAGGACACCCGGGCTCTGCAAC 1805
1670 TGGGACATCTGTTCTGTACCTGTGGAGGAGGTACAGAAAGTAGTGTCTCTGCAAC 1729
1806 AGCCCTGAGCTCAGTACGAGGAGGAGGCTGCTGGGGATGTGAGAGGCTCAGATG 1865
1730 AACCCACACCCAGTTTGGAGCAAGGACTGCGTTGGTGTATTAACAGAAACACAGATC 1789
1866 TGCAACAAGAGGAGTGCCTCCGCTGGATGCTGTTTATCAACCCCTGCTCCCGGAGCC 1925
1790 TGCACACAGAGACATGTCATTAATGATGATGCTGTCCATCCCTGCTTGGCCGGTG 1849
1926 CAGTCAGCAGCTTCCCGATGGCTGCTGTGTCATGCGGCTTCTGCCCTGTGGGCTTCTTTC 1985
1850 AAGTGTACTAGCTACCTGATGACCTGGAATGTGGTGTGTCCTCCCTGTTACAGT 1909
1986 GGCATTTGGACCACTGTGAGGACCTGGAGAGTGTGCCCTGGTCCCGACATCTGCTTC 2045
1910 GGAATTTGGATCCAGTGCACAGATGTGATGATGATGATGATGATGATGATGATGATG 1969
2046 TCCACCAAGAGTGCCTGCTGCTGTCAACTCAGCTGACCTGGCTTCCACTGCTGCTGCTTC 2105
1970 AACCAATTTGGAGACACCGGTGTGAGACACGGACCCCGGCTTACAACTGCTGCTGCTTC 2029
2106 CGCCCGGATACAGAGGAAACAGCCGCTCGGGTGTGAGGCTGGAAGCAGCAGCGGAA 2165
2030 CCCCACGCTTACCGGCTCAGACCCCTTGGCCAGGCTGTGAGATGCGCAGCGGCAAC 2089
2166 AAGCAAGTGTGAGGCCGAAACCCATGCAAGGACAGACACACAACTGCCACAGCAC 2225
2090 AAACAGCTGTGAAGCCCGTAAACCCCTGACGGATGGGACCCACAGCTGCAACAGAAC 2149
2226 GGGAGTGTATCTACCTGGTCACTTACAGGACCCATGACAGTGGAGTGGCAGACA 2285
2150 GCAAGTGTACCTGCTGGCCACTATAGCAGCCCATGTACCGCTGCGAGTGCAGGCT 2209
2286 GGTACGCGGGGACGGGCTCATCTGCGGGGAGGACTCGGACCTTGACGCGCTGGCCCAAC 2345
2210 GGCTAGCTGGCAATGGCATCATCTGCGGGAGGACACAGACCTGGATGGCTGGCCAT 2269
2346 CTCATCTGCTGCGCCACCAAGCCACTACACTGTATCAAGATCAAGATCAAGTGCCTTAC 2405
2270 GAGAAGCTGGTGTGGTGGCCCAATGCGACTTACCACTGCAAAAAGGATAATTGCCCAAC 2329
2406 CTGCCAAATCTGGGAGGAGACTTTGACAGGAGCGGATGGGATGCTGTGATGAT 2465
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2466 GAGATGACAATGACGGTGTGACCATGAGAGGACAACTGGCAGCTCTCTTCAATCC 2525
2390 GAGGATGACAATGATAAATTCAGATGACAGGACAACTGTCCATTCAATTAACACCA 2449
2526 CGCAGGCTGACTATGACAAAGATGAGGTGGGACCGCTGTGACAACTGCCCTTACGTC 2585
2450 GCTCAGTATGACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACTGTCCCTACAC 2509
2586 CACAACTTCCAGATCAGACAGACAACTGAGAGGCTGAGCCTGCTCCGTGGAC 2645
2510 CACAACCCAGATCAGCGAGACACACAACTGAGGAGGAGCGCTGTGCTGACAG 2569
2646 ATTGATGGGAGGATGCTTCAATGAACGAGACAATTTGCCCTAGCTCTACAACTAG 2705
2570 ATTGATGAGAGCGTATCTCAATGAACGGGACAACTGCCAGTACTACATGTGAC 2629
2706 CAGAGGGACACGGATGGTACCGGTGTGGGGATCACTGTGACAACTGCCCTGTGTCAC 2765
2630 CAGAGAGACACTGATGATGGATGGGTGTGGAGATCAGTGTGACAATTTGCCCTTGAACAC 2689
2766 AACCTTGACCAACCGAGTGCACAACTGCTGTTGGGACCACTGTGACACACAGCAG 2825

2690 AATCCGGATCAGCTGACGCTCTGACTCAGACCGCATTTGGAGATACCTGTGACACAAATCAG 2749
2826 GACATAGATGACGACGGCCACAGAAACACCAAGGACAACTGCCCCATCTCTCAACGCC 2885
2750 GATATTGATGAAGATGCGCCACAGAACTCTGGACAACTGTCCTTATGTGCCAATGCC 2809
2886 AACCAGGCTGACATGACAGAGACGGCCAGGGGAGCGCTGTGACCTGTGATGATGACAA 2945
2810 AACCAGGCTGACATGACAAAGATGGCAAGGAGATGCTGTGACCAAGATGATGACAA 2869
2946 GATGGCTGCCGATGACAGGAGCACTGCGGCTTGTCTCAACCCAGACAGGAGGAC 3005
2870 GATGGATTTCCGATGACAGGACAACTGACACTCGTGCCCAATCCCGACCAAGAGAC 2929
3006 TTGGAGGCTGATGAGCGGGTGATATTTGTAAGATGATTTTACAAATGACAACTCCCA 3065
2930 TCTGAGCGGATGGTTCGAGGTGATGCTGCAAGATGATTTTGACCATGACAGTGTGCCA 2989
3066 GATATTGATGATGTGTCTCTGAAACAAATGCCATCAGTGAGACAGACTTCAGGAACCTTC 3125
2990 GACATCGATGACATCTGCTCTGAGAATGTGACATCAGTGAGACCGACTTCCGCCGATTC 3049
3126 CAGATGGTCCCTGATCCCAAGGAGCACCCAAATTTGATCCCAACTGGGTCACTCC 3185
3050 CAGATGATTTCTTGACCCCAAGGAGACATCCCAAAATGACCCCTAACTGGGTGTACGC 3109
3186 CATCAAGGCAAGGAGTGGTTCAGACAGCAACTCGGACCCCGGATCTGCTAGGTTC 3245
3110 CATCAGGTTAAGAACTCTCTCAGACTGTCAACTGTGATCTCTGGACTCGCTGTAGTTAT 3169
3246 GACGAGTTTGGTCTGTGGACTTCAGTGGCACATTTCTAGTAAACACTGACCGGGACGAC 3305
3170 GATGAGTTTAAATGCTGTGGACTTCAGTGGCACCTTCTCATCAACACCCGAAAGGACGAT 3229
3306 GACTATGCTGGCTGCTGCTTGGTTACAGTCAAGCAGCGCTTCTATGTGTGATGTGG 3365
3230 GACTATGCTGGATTTGTCTTGGCTACAGTCCAGACCGCTTTATTTGTGTGATGTGG 3289
3366 AAGCAGGTCGACGACCTTACTTGGGAGGACACGACCGCGCTTATGGCTACTCCGCGC 3425
3290 AAGCAAGTCACCCAGTCTCTTGGACACCAACCCACAGGGCTCAGGATACTCGGCG 3349
3426 GTGTCTCTCAAGGTGGTGAATCTCCACGAGGGAGCGGGAGACCTGAGGAACGGCTG 3485
3350 CTCTTGTGAAAGTTGTAAACTCCACACAGGGCTTGGCGAGCACTGGCGAACCGCTG 3409
3486 TGGCACACGGGAACACCGCGGCGAGGTGCGAACTTATGCGACGACCCAGGAACAT 3545
3410 TGGCACACAGGAACACCCCTGGCCAGGTGCGCACCCCTGTGGCATGACCTCGTCACATA 3469
3546 GGCTGGAAGGACTACACGCGCTTATAGTGGCACCTGACTCAGAGCCCAAGACCGCTAC 3605
3470 GGCTGGAAGATTTACCGCTCTACAGATGGCTCTCAGCCACAGCCCAAGACGGTTTC 3529
3606 ATCAGAGTCTTAGTGCATGAAGGAACAGGTGATGGCAGACTCAGGACCTATCTATGAC 3665
3530 ATTAGAGTGTGATGATGAAGGAAGAAATCATCGCTGACTCAGGACCCATCTATGAT 3589
3666 CAAACCTTACGCTGCGCGGCTGGTCTATTTGTCTTCTCTCAAGAAATGCTCTATTC 3725
3590 AAAACCTATGCTGGGTAGACTAGGTTGTGTTCTTCTCTCAAGAAATGCTGTCTTC 3649
3726 TCAGACCTCAAGTACGAATGACAGATATTTAAACAAGATTTGCTGCAAT 3775
3650 TCTGACCTGAATAGCAATGATAGATCCCTAATCATCAATTTGTTGAT 3699

RESULT 7
US-09-925-301-205
; Sequence 205, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

;; FILE REFERENCE: PA106

;; CURRENT APPLICATION NUMBER: US/09/925,301

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: PCT/US00/05882

;; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270

;; PRIOR FILING DATE: 1999-03-12

;; NUMBER OF SEQ ID NOS: 1694

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 205

;; LENGTH: 5830

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: misc_feature

;; LOCATION: (5584)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc_feature

;; LOCATION: (5585)

;; OTHER INFORMATION: n equals a,t,g, or c

;; NAME/KEY: misc_feature

;; LOCATION: (5821)

;; OTHER INFORMATION: n equals a,t,g, or c

;; US-09-925-301-205

Query Match 26.4%; Score 1529.8; DB 10; Length 5830;
Best Local Similarity 65.8%; Pred. No. 0;
Matches 2325; Conservative 2; Mismatches 1169; Indels 35; Gaps 6;

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QY 252 CTGCTCTGCTGGCTGTGGTGTGGCCAGCAGCAAGCTGCTCACCAGGACAAGAC 311
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DB 187 CTGTTCTGTGATGCTGTGGTGTGGCCAGCAACCGCATTCAGAGTCTGGCGGAGACA 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 312 ACGACCTTCGACCTTTTCAGTATCAGCAACATCAACCGCAAGACCATTTGGCGCCAAAGCAG 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 AGCGTGTGTGACATCTTGAACCTCACCGGGCCGCCGCAAGGGTCTGGCGCCGACTG 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 372 TTCGGCGGGCCGACCCGGGGTCCGGCTTACCGTTTACCGTTTGGCGCTTTGACTACATCCCA 431
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 304 GTGAAGGGCCCGCCCTTCAGCCAGCTTCCAGCCAGCTTCCGGCATCGAGGATGCCAACCTGATCCC 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 CCGGTGAAGCGAGATGACCTCAGCAAGATCACCAGATCATCGCGCAGAGGAGGGCTTC 491
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 364 CCTGTGCTGTATGACAGTTCACAGACCTGTGTGATGCTGTGGGCGAGAAAGGGTTTC 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 492 TTCCTCAGCGCCAGCTCAAGCAGGAGCGCAAGTCCAGGGCGACGCTTTGGCTCTGGAG 551
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 424 CTCCTTCTGGCATCCCTGAGGCATGAGAGACACCGGGCGACGCTGTGGCCCTGGAG 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 552 GGCCCGGGTCTCTCCAGAGCAGTTCGAGATCTCTCCACAGCCCGCCCGGACACGCTG 611
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 484 CGGAAGAACCACTCTGGCCAGCTTTCAGCGTGGTGTCCATGCAAGCGGGCACCCCTG 543
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 612 GATCTCAGCTACTGATTTAGCGGCACCGGCATGTGCTCTCCCTGGAGGAGTCCGGCTG 671
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 GACCTCAGCTTACCGTCCAGGAACAGCAGCAGTGTGTGTGGGAAGAGCTCTCCCTG 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 672 GCTGACTCGCAGTGGGAAGAGCTCACCGTGCAGGTGGCTGGCGAGACCTACAGCTTGCAC 731
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 GCAACCGGCAGTGGAGAGCATCACCTGTTTGTGCAGGAAGACAGGGCCACCTGTAC 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 732 GTGGGCTGCGACCTCATTAGGACAGTGTCTCTGGACGAGCCCTTCTACGAGCAGCTGCAG 791
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 664 ATCAGCTGTGAAAAGATGGAGATGCTGAGTTGGACGTCCCATCCAAAGCGCTTCAAC 723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 792 GCGAAAAGAGCCGATGATAGTGGCCAAAGGCTC-----TGCCAGAGAGTCACTTC 845
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 724 AGAGCTTGGCCAGCATCGCCAGACTCCGCATCGCAAGGGGGCGCTCAATGACAATTC 783
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 846 AGGGTTTGTTCAGAACCTCCACCTAGTGTGTTTGAAGAACTCTGTGGGAAGATATTCTAAGC 905
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 784 CAGGGGTGCTGCAGATGTGAGGTTTGTCTTTGGAAACACACACAGAGACATCCTCAGG 843
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-140

Query Match      10.4%; Score 601.6; DB 9; Length 2439;
Best Local Similarity 63.1%; Pred. No. 5.1e-133;
Matches 947; Conservative 0; Mismatches 544; Indels 9; Gaps

Qy 2254 GCGACCCCATGTATAAGTGCAGATGCCAGACAGAGGTACGGCGGACGGGCTCATCTGCG 2313
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 765 GCGATGGCTCGCGTGTGCGTGTGCGGTTGGCTGGCGCGCAACGGGATCCTCTGTG 824

Qy 2314 GGGAGGACTCGGACTCGGAGGCGTGCCTCAACTCAATCTGGTCTGCCCCACCAACAGCCA 2373
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 825 GTCCGACACTGACCTAGACGCGCTCCCGGAGCAGAAGCTGCGCTGCCCGGAGCGC---- 880

Qy 2374 CCTACCACCTGCATCAAGGATAACTGCCGCCCATCTGCCAAATCTGGGCGAGGAAGACTTTG 2433
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 881 -----CAGTCCCTAAGACAACTGGGTACTGTGCCCAACTCAGGCGCAGGAGATGTGG 935

Qy 2434 ACAAGACGGGATTGGCGATGCTGTGTATGATGACGATGACAATGACGGTGTGACCGGATG 2493
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 936 ACCGCGATGATCGGAGACGCTCGGATCCGGATGCCGACGGGACGGGTCCCCCAATG 995

Qy 2494 AGAAGACAACCTGCCAGCTCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGG 2553
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 996 AAAAGGACAACCTCCCGCTGGTGGGAACCCAGACGCGCAACACGGACGACGACAAAGT 1055

Qy 2554 TTGGGACCGCTGTGACAACCTGCCCTTAGCTGCACAACCCCTGCCAGATCCACACAGACA 2613
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1056 GGGCGCATGCGTGGCAACTGCGCGTCCCAAGAAACAGACGACCAAAAGGACACAGACC 1115

Qy 2614 ACAATGAGAGGCTGACGCGCTGCTCGTGGCACTTGTATGGGACGATCTCTTCAATGAAC 2673
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1116 AGNAGCGCGGGCGATGCGTGGGACGACGACATCGACGGCGACCGGATCCGCACACG 1175

Qy 2674 GAGACAATTTGCCCTACGCTTAAACAATGACACGAGGACACAGGATGGTACGCTGTGG 2733
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1176 CCGACAACCTGCCCTAGGGTACCCAATCAGACGAGGACAGATGATGGCGATGATAG 1235

Qy 2734 GGGATCACTGTGACAACCTGCCCTGGTGCACAACCCCTGACGACACGACGATGGACAAATG 2793
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1236 GGGATGCTGTGACAACCTGCCCAAGAGAACACCCCGGATCAGGCGGATGTGGACCAAG 1295

Qy 2794 ACCTTGTGGGGACAGTGTGACAACACGAGGACATAGATGACGACGGCCACCAAGACA 2853
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1296 ACTTTGTGGAGATGCTTGTGACAGGGATCAGACACGAGTGGAGACGGACATCAGGACT 1355

Qy 2854 ACCAGGACAACCTCCCTACATCTCCAACGCCAACCCAGGCTGACCATGACAGACGCGCC 2913
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1356 CTCGGGACAACCTGCCACGGTGCCTAACAGTGGCCACGAGGAGACTCAGACCAACGATGCC 1415

Qy 2914 AGGGCAGCGCTGTGACCTGTATGATGACAACGATGGCTGCCCGATGACAGGAGCAACT 2973
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1416 AGGTGATGCTCTCGACGACGACGACGACAATGACGGAGTCCCTGACAGTCCGGACAAC 1475

Qy 2974 GCGGCTGTGTCAACCCAGACACGAGGAGACTTGGACGCTGTATGGACGGGTGATATTT 3033
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1476 GCGGCTGTGTGCCCTAACCCCGCAGGAGGACCGGACAGGACGCGCTGGGCGACGCTGT 1535

Qy 3034 GTAAAGATGATTTTGACAATGACAACATCCCAAGATTTGATGATGTGTCTCTGCTGAAACA 3093
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Db 1536 GCCAGGACGACTTTGATGCAGACAGGTGTTAGACAAGATCGAGCTGTGTCCGGAGAACG 1595

Qy 3094 ATGCCATCAGTGAGACAGACTTCAGGAATCTCCAGATGGTCCCTTGATCCCAAGAGGA 3153
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1596 CTGAAGTACGCTCACCGACTTCAGGGCTTCCAGACAGTCTGTGTGACCCGAGGCTGT 1655

Qy 3154 CCACCCAAATTTGATCCCACTGGGTCAATTCGCCATCAGGCAAGGAGCTGTTCAGACAG 3213
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1656 ACCGCAGATTTGACCCCACTGGGTGGTGCTCAACAGGGGAAGGAGATCTGTGACACA 1715

Qy 3214 CCAACTCGGACCCCGGCATCGCTGTAGTGTGAGGCTTTTGACGAGTTTGGGTCTGTGCACTTCACTG 3273

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| Db | 1716 | TGAACAGCGACCCAGAGCCCTGGCTGTGGGTTACACTGCCTTCAATGGCGCTGGACTTCGAGG | 1775 |
| Qy | 3274 | GCACATTTCTAGCTAAACACTTGACCGGGAGCGAGCACTATGCTGGCTTCGCTCTTGGTTACC | 3333 |
| Db | 1776 | GCAGTTTCCATGTGAACACGGTACCGGATGACGACTATCGGGCGTTTCATCTTTGGCTACC | 1835 |
| Qy | 3334 | AGTCAAGCAGCCGCTTCTATGTGTGTGATGTGGAAGCAGGTGACGACAGCACTACTGGGAGG | 3393 |
| Db | 1836 | AGGACAGCTCCAGCTTCTACGTGGTTCATGCTGGAAGCAGATGGAGCAACAGTATTGGCAGG | 1895 |
| Qy | 3394 | ACAGCCCGACCGGGGCTATGCGCTACTCCGGCGTGTCCCTCAAGGTGGTGAACCTCCACCA | 3453 |
| Db | 1896 | CGAACCCCTTCCGTGCTGTGGCGAGCCCTGGCATCCAACCTCAAGGCTGTGAAGTCTTTCCA | 1955 |
| Qy | 3454 | CGGGGAGGGCGAGCAGCTTGAAGACGGCTGTGGCACACGGGGAACACGCCGGGGCAGG | 3513 |
| Db | 1956 | CAGGCCCCGGGGAAACAGCTCGCGAAGCGTCTGTGGCATACAGGACACAGAGTCCCCAGG | 2015 |
| Qy | 3514 | TGGCAACCTTATGGCACGACGCCCGAGGAACATTTGGCTTGAAGGACATACACGGCGCTATAGGT | 3573 |
| Db | 2016 | TGCGGCTGCTGTGGAGGAGCCCGGAAACGCTGGTTGGNAGCAAGAGTCTCTATCGTT | 2075 |
| Qy | 3574 | GGCACTTGACTCACAGGCCCCAAGACCGGCTACATCAGAGTCTTTAGTGCATGAAGGAAAC | 3633 |
| Db | 2076 | GTTTCTTGACAGCAGCGGCCCAAGTGGGCTACATCAGGCTGGGATCTTATGAGGCCCTG | 2135 |
| Qy | 3634 | AGGTGATGGCAGACTCAGGACCTATCTATGACCAAACTACGCTGGCGGGCGGTGGGTC | 3693 |
| Db | 2136 | AGCTGTGGCGCAGACGAACAGTGGTCTTGGACACAACCATGCGGGGTGGCGCCCTGGGGG | 2195 |
| Qy | 3694 | TATTTGTCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATGCCAGAGATA | 3753 |
| Db | 2196 | TCCTCTGCTTCTCCAGGAGAACATCATCTGGGCCAACCTCGCTTACCGCTGCAATGACA | 2255 |
| RESULT 9 | | | |
| US-09-954-531-359 | | | |
| ; Sequence 359, Application US/09954531 | | | |
| ; Patent No. US20020165180A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: weaver, Zoe | | | |
| ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agen | | | |
| ; TITLE OF INVENTION: Gene Sets | | | |
| ; FILE REFERENCE: 689290-77 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/954,531 | | | |
| ; CURRENT FILING DATE: 2002-05-02 | | | |
| ; PRIOR APPLICATION NUMBER: US/60/233,133 | | | |
| ; PRIOR FILING DATE: 2000-09-18 | | | |
| ; PRIOR APPLICATION NUMBER: US/60/234,009 | | | |
| ; PRIOR FILING DATE: 2000-09-20 | | | |
| ; PRIOR APPLICATION NUMBER: US/60/234,034 | | | |
| ; PRIOR FILING DATE: 2000-09-20 | | | |
| ; PRIOR APPLICATION NUMBER: US/60/234,509 | | | |
| ; PRIOR FILING DATE: 2000-09-22 | | | |
| ; PRIOR APPLICATION NUMBER: US/60/234,567 | | | |
| ; PRIOR FILING DATE: 2000-09-22 | | | |
| ; NUMBER OF SEQ ID NOS: 1392 | | | |
| ; SOFTWARE: PatentIn version 3.0 | | | |
| ; SEQ ID NO 359 | | | |
| ; LENGTH: 2439 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| US-09-954-531-359 | | | |

| | | | | | | | | |
|----|-----------------------|--|--------------|---------------|------------|------|--------|---------|
| | Query Match | 10.4% | Score | 601.6; | DB | 9; | Length | 2439; |
| | Best Local Similarity | 63.1%; | Pred. | No. 5.1e-133; | | | | |
| | Matches | 947; | Conservative | 0; | Mismatches | 543; | Indels | 9; Gaps |
| Qy | 2254 | CGCAGCCCATGTACAAGTGCAGTGCCGACAGAGCTACGCCGGGACGGGCTCATCTCGG | 2313 | | | | | |
| Dd | 765 | GCGATTGGCTCGGGTGTTCGTCGTGTGTCCGTTGGTGGCCGCAACGGATCCCTCTGTG | 824 | | | | | |

QY 2314 GGGAGGACTGGGACCTGGAGCGTGGCCCAACCTCAATCTGGTCTGCGCCACCAAGCCCA 2373
Db 825 GTGCGACACTGACCTAGAGCTGCTCCGAGGAGAAAGTGGCTGCGTCCCGGAGCCG- --- 880
QY 2374 CTTACCACTGCATCAAGGATAACTGCCCCATCTGCCAAATCTGGCGAGGAAGACTTGG 2433
Db 881 -----CAGTGGCGTAAGGACAACTGGGTGACCTGTCGCCCAACTCAGGCGAGGAGGATGTGG 935
QY 2434 ACAAGGAGGGATGGCGATGCTGTGATGATGACGATGACAAATGACGGTGTGACCGATG 2493
Db 936 ACCGCGATGGCATCGGAGACGCTGCGATCGGATCGCGACGGGACGGGGTCCCAATG 995
QY 2494 AGAAGGACAACTGCCAGCTCTCTCAATCCCGCCAGCTGACTATGACAAGGATGAGG 2553
Db 996 AAAAGGACAACTGCCCGCTGGTGGGAACCCAGACGCGCAACACGGAGGAGCAAGT 1055
QY 2554 TTGGGACCGCTGTGACAACTGCCCTTAGCTGCACAAACCTGCCAGATCGACACAGACA 2613
Db 1056 GGGCGATGGTGGGCAACTGCCGTCCAGAGACAGACGACCAAAAGGACACAGACC 1115
QY 2614 ACAATGAGAGGGTACGCGCTCTCCGTGGACATGATGGGACGATGCTCTTCAATGAAC 2673
Db 1116 AGGACGCGCGGGCGATGGTGGACGAGACATCGACGGCGACCGGATCCGCAACCCAGG 1175
QY 2674 GAGACAAATGTCCCTACGCTCTACACACTGACACAGGAGACAGGATGTGACGGTGG 2733
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QY 2794 ACCTTTTGGGACCACTGTGACAAACAGGAGGACATGATGACGACGCGCCACCAAGACA 2853
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Db 1356 CTCGGGACAACTGTCCCGGTGCTTACAGTGCACAGGAGGACTCAGACCAACGATGGCC 1415
QY 2914 AGGGGACCGCTGTGACCTGATGATGACAAAGGATGGCGTCCCGATGACAGGACAACT 2973
Db 1416 AGGGTATGCTTGCAGCGACGACGACAAATGACGGATCCCTGACAGTCCGGACAACT 1475
QY 2974 GCGCGTGTGTTCAACCCAGCAGGAGGACTTGGAGGATGATGACGCGGGTGTATTT 3033
Db 1476 GCGCGTGTGCTTAACCCCGCCAGGAGGACGCGACAGGACGCGGTGGCGCGAGTGT 1535
QY 3034 GTAAAGATGATTTGACATGACAACTCCAGATATTGATGATGTGTCTGAAACA 3093
Db 1536 GCGAGGACACTTTGATGACAGAAAGGTTGATAGAAAGATGACGATGTGTCCGAGAAAG 1595
QY 3094 ATGCCATGATGAGACAGACTTCAGGAATTCAGATGGTCCCTTGGATCCCAAGGA 3153
Db 1596 CTGAAGTACGCTACCGACTTCAGGGCTTCCACAGCTGCTGACCCCGAGGGTG 1655
QY 3154 CCACCCAAATGATCCCACTGGGTATTCGCCATCAAGGCAAGGAGCTGTTCAGACAG 3213
Db 1656 AGCGCGAGATTCACCCCAACTGGGTGTCTCAACAGGGAAGGAGATCGTGACAGACA 1715
QY 3214 CCAACTCGGACCCCGCATCGTGTAGTTTACAGATTTGGGTCTGTGACTTCAGTG 3273
Db 1716 TGAACAGGACCGCGCTGGCTGTGGTTTACACTGCTTCAATGGCGTGGACTTCGAGG 1775
QY 3274 GCACATTTCTACATAAACAACACTGACCGGAGCAGCTATGCTGGCTTCTTTGGTTACC 3333
Db 1776 GCACGTTCCATGTGAACCGGTTCAGGATGACGACTATCGGGCTTCATCTTTGGCTACC 1835
QY 3334 AGTCAAGCAGCGCTTCTATGTGTGATGTGGAAGCAGGTGACGACGACCTACTCGGAGG 3393
Db 1836 AGGACAGCTCCAGCTTCTACGTGGTGTGATGTGGAAGCAGATGAGCAACAGTATTGGCAGG 1895
QY 3394 ACCAGCCCAAGCGGCGCTATGGCTACTCGGCGCTGTCCCTCAAGGTGGTGAACCTCCACA 3453

Db 1896 CGAAACCCCTTCGCTGCTGTGGCCGAGCCTTGGCATCAACTCAAGCTGTGAAGTCTTCCA 1955
QY 3454 CGGGGACGGCGAGCACTTGAAGAAACGCGCTGTGGCACACGGGGAACACGCGGGGCGAG 3513
Db 1956 CAGGCGCGGGGAACAGCTGTGGGAACGCTCTGTGCAATACAGGACACAGAGTCCGAG 2015
QY 3514 TCGCAACCTTATGGACGACCCAGGAACATTTGGCTGGAAGACTACAGCGCTATAGGT 3573
Db 2016 TCGCGCTGCTGTGAAGGACCGCCGAAACGCTGGTGTGAAGGACAAGAGTCTATCGTT 2075
QY 3574 GCACTGACTACAGGCGCAACAGCCGCTACATCAGAGTCTTAGTGCATGAAGAAAC 3633
Db 2076 GTTCTCTGACAGCGCGCCCAAGTGGCTACATCAGGCTGCGATTTCTATGAGGCCCTG 2135
QY 3634 AGGTCATGCGACACTCAGGACCTATCTATGACCAAAACCTACGCTGGCGGGCGGTG 3693
Db 2136 AGCTGGTGGCGACAGCAACGCTGTGTCGACACAAACCATCGGGGTGCGCCCTCGGG 2195
QY 3694 TATTTGCTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAATCGAGATA 3753
Db 2196 TCTTCTGCTTCTCCAGGAGACATCTCTGGGCCAACCTGCGTTACCGCTGCAATGACA 2255
RESULT 10
US-10-025-380-327/c
; Sequence 327, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Mesgher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yudi
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 327
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 137..490, 493
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-327

Query Match 10.3%; Score 595.6; DB 9; Length 619;
Best Local Similarity 98.7%; Pred. No. 5.6e-132;
Matches 609; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 4190 TTAAGTTGTGCATATTTCTTGAATAGAGTTGCTTCAATGACACACAAATCCG-GCTA 4248
Db 617 TAAAGTTGTGCATATTTCTTGAATAGAGTTGCTTCAATGACACACAAATCCGCGCTA 558
QY 4249 AATAAATATTAACCAAGGTCGAATTTCAATTTGAAGTAAATTTAGTAAAGGAGATTA 4308
Db 557 AATAAATATTAACCAAGGTCGAATTTCAATTTGAAGTAAATTTAGTAAAGGAGATTA 498

Query Match 10.3%; Score 595.6; DB 10; Length 619;
 Best Local Similarity 98.7%; Pred. No. 5.6e-132;
 Matches 609; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 4190 TTAAGTTGTCACATTTCTTGAATTAGAGTGTCTCTACAAATGACACACAAATCCC-GCTA 4248
 Db 617 TAAAGTTGTCACATTTCTTGAATTAGAGTGTCTCTACAAATGACACACAAATCCC-GCTA 558
 QY 4249 AATAAATTATAAACAAGGTCATTTCAAAATTTGAAGTAATGTTTAAAGGAGAGATTAA 4308
 Db 557 AATAAATTATAAACAAGGTCATTTCAAAATTTGAAGTAATGTTTAAAGGAGAGATTAA 498
 QY 4309 GAAGACAACAGGATAGCAAAATGACATAAGCTACCATTAACTAATCGGAACATGTAAAA 4368
 Db 497 GAAGNCTNAGGATAGCAAAATGACATAAGCTACCATTAACTAATCGGAACATGTAAAA 438
 QY 4369 CAGTTACAAAATAAACAAGCTCTCTCTGTCCTTACAAATGAAGCCCTCATGTCCAGTA 4428
 Db 437 CAGTTACAAAATAAACAAGCTCTCTCTGTCCTTACAAATGAAGCCCTCATGTCCAGTA 378
 QY 4429 GAGATCAGTTTTCATCAAAAGAACAAACATCTTGGCAAATGGGTGTGACCGGTTCAGAT 4488
 Db 377 GAGATCAGTTTTCATCAAAAGAACAAACATCTTGGCAAATGGGTGTGACCGGTTCAGAT 318
 QY 4489 GTGGATTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGACAAAGTGGGTGCTTTAG 4548
 Db 317 GTGGATTGGCAAAACCTCATTTAAGTAAAGGTTAGTACAAAGGTTAGTACAAAGTGGGTGCTTTAG 258
 QY 4549 GTGCTGCTTGTGCGGTGTGGCGTGGGGAGGCTCTGCTGCTGAGCTTCCTTCCCGAGCTT 4608
 Db 257 GTGCTGCTTGTGCGGTGTGGCGTGGGGAGGCTCTGCTGCTGAGCTTCCTTCCCGAGCTT 198
 QY 4609 TGCTGCTGAGAGAACACAGACAGCAGCGCAGCGGCGGAAAAAGGGCGATCTAACGCGTAT 4668
 Db 197 TGCTGCTGAGAGAACACAGACAGCAGCGCAGCGGCGGAAAAAGGGCGATCTAACGCGTAT 138
 QY 4669 CTAGGCTTTGGTAACGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCAATTA 4728
 Db 137 NTAGGCTTTGGTAACGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCAATTA 78
 QY 4729 GGTTCAGTTATAATATTTTCTTAATTTTAAATTTAAGTACATATAGATGCAACTCCATT 4788
 Db 77 GGTTCAGTTATAATATTTTCTTAATTTTAAATTTAAGTACATATAGATGCAACTCCATT 18
 QY 4789 TACCAGTAACTTATTTT 4805
 Db 17 TACCAGTAACTTATTTT 1

RESULT 13
 US-09-815-343-1448/c
 ; Sequence 1448, Application US/09815343
 ; Patent No. US20010055596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meagher, Madeleine
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: King, Gordon E.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 210121.504
 ; CURRENT APPLICATION NUMBER: US/09/815,343
 ; CURRENT FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 1556
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1448
 ; LENGTH: 637
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(637)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-815-343-1448
 Query Match 9.3%; Score 540.2; DB 10; Length 637;
 Best Local Similarity 94.9%; Pred. No. 8.6e-119;
 Matches 595; Conservative 0; Mismatches 28; Indels 4; Gaps 4;

QY 4182 TTTGGTGTAAAGTTGTACATTTCTTGAATTTAGAGTGTCTCTACAAATGACACACAAAT 4241
 Db 626 TTTTGGTGTAAAGTTGTCTCCTTATTTNTGAATAAGAGTTGTTC-NCAATNACACCAAT 568
 QY 4242 CCGCTAATAATATTAACAAGGTCATTTCAAAATTTGAAGTAATGTTTGTAGT-AAG 4299
 Db 567 TCCNGTAAATAATATTAACAAGGTCATTTCAAAATTTGAAGTAATGTTTGTAGTAAAG 508
 QY 4300 GAGATTTAGAAAGACAGGATAGCAAAATGAC-ATAAGCTACCGATTTAACTAATCGGA 4358
 Db 507 GAGATTTAGAAAGACAGGATAGCAAAATGACAAATGACAAATGACAAATCGGA 448
 QY 4359 ACATGTAACAGTTTACAAAAATAAACGAACTCTCTCTGCTGTCTACAAATGAAGCCCTC 4418
 Db 447 ACATGTAACAGTTTACAAAAATAAACGAACTCTCTCTGCTGTCTACAAATGAAGCCCTC 388
 QY 4419 ATGTGCACTAGAGATGCAAGTTTCATCAAGAACAAACATCTCTGCAATGGGTGTGACGC 4478
 Db 387 ATGTGCACTAGAGATGCAAGTTTCATCAAGAACAAACATCTCTGCAATGGGTGTGACGC 328
 QY 4479 GGTTCACAGTGTGGATTTGGCAAAACCTCATTTAAGTAAAGTAAAGGTTAGCAGACAAAGTGC 4538
 Db 327 GGTTCACAGTGTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGACAAAGTGC 268
 QY 4539 GGTGCTTTAGCTGTGCTGTGCTGCTGTGCGGTGGGGAGGCTCTCTGCTGAGTTCCT 4598
 Db 267 GGTGCTTTAGCTGTGCTGTGCTGCTGTGCGGTGGGGAGGCTCTCTGCTGAGTTCCT 208
 QY 4599 TCCCGAGCTTGTGCTGCTGAGAGAACAGCAGCAGCAGCAGCGGCGGAAAAAGGCGCATC 4658
 Db 207 TCCCGAGCTTGTGCTGCTGAGAGAACAGCAGCAGCAGCAGCGGCGGAAAAAGGCGCATC 148
 QY 4659 TAACGCGTATCTAGGCTTTGGTAACTGGGCAAGTGTGCTTTTACCTGATTTGATGATAC 4718
 Db 147 TAACGCGTATCTAGGCTTTGGTAACTGGGCAAGTGTGCTTTTACCTGATTTGATGATAC 88
 QY 4719 ATTTCATTAAGTTCCAGTTATAAATATTTGTTAATTTAATTAAGTACATTAAGAATG 4778
 Db 87 ATTTCATTAAGTTCCAGTTATAAATATTTGTTAATTTAATTAAGTACATTAAGAATG 28
 QY 4779 CAATCCATTTACCAGTAACTTATTTT 4805
 Db 27 CAATCCATTTACCAGTAACTTATTTT 1

RESULT 14
 US-09-920-300A-1233
 ; Sequence 1233, Application US/09920300A
 ; Patent No. US20020136728A1
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.547
 ; CURRENT APPLICATION NUMBER: US/09/920,300A
 ; CURRENT FILING DATE: 2001-07-31
 ; NUMBER OF SEQ ID NOS: 1789
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1233
 ; LENGTH: 516
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: n = A,T,C or G

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 8.9% | Score 516; | DB 10; | Length 516; |
| Best Local Similarity | 100.0%; | Pred. No. 4.3e-113; | | |
| Matches 516; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
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| QY | 4057 | AAAAAGAATGACGTTCACATATAAAATGTAATTACTTATTCTATTATTCTATTATTTATGCTATATGGAG | 4116 |
| Db | | 1 AAAAAGAATGACGTTCACATATAAAATGTAATTACTTATTCTATTATTCTATTATTTATGCTATATGGAG | 60 |
| QY | 4117 | TTGAAAGGAATPACTGTGCATAAGCCATTATGATAAAATTAAGCATGAATAATATTGCTGAA | 4176 |
| Db | | 61 TTGAAGGGAATPACTGTGCATAAGCCATTATGATAAAATTAAGCATGAATAATATTGCTGAA | 120 |
| QY | 4177 | CTACTTTTTGGTGCTTAAGTTGTCACATATCTTGAATTAGAGTTGCTCTACAATGACACA | 4236 |
| Db | | 121 CTACTTTTTGGTGCTTAAGTTGTCACATATCTTGAATTAGAGTTGCTCTACAATGACACA | 180 |
| QY | 4237 | CAAAATCCCGCTAAATAAATATATAACAAGGCTCAATTCAAATTTGAAGTAATGTTTTAGT | 4296 |
| Db | | 181 CAAAATCCCGCTAAATAAATATATAACAAGGCTCAATTCAAATTTGAAGTAATGTTTTAGT | 240 |
| QY | 4297 | AAGGAGAGATTAGAAGACACACAGGCATAGCANAATGACATAAGCTACCAGATTAACTAATCG | 4356 |
| Db | | 241 AAGGAGAGATTAGAAGACACACAGGCATAGCANAATGACATAAGCTACCAGATTAACTAATCG | 300 |
| QY | 4357 | GAACATGTFAAACAGTTACAAAAATAAACGAACTCTCCTCTGTGCTTACAAATGAAGCCC | 4416 |
| Db | | 301 GAACATGTFAAACAGTTACAAAAATAAACGAACTCTCCTCTGTGCTTACAAATGAAGCCC | 360 |
| QY | 4417 | TCATGTGCAGTAGAGATGCAGTTTTTCATCAAAAGAACAAACATCCTTGGAAAATGGGTGTGAC | 4476 |
| Db | | 361 TCATGTGCAGTAGAGATGCAGTTTTTCATCAAAAGAACAAACATCCTTGGAAAATGGGTGTGAC | 420 |
| QY | 4477 | GCGETTCCAGNTGGGATTGGGCCAAAACCCATTTAAGTAAAGGTTAGCAGAGCAAGT | 4536 |
| Db | | 421 GCGETTCCAGNTGGGATTGGGCCAAAACCCATTTAAGTAAAGGTTAGCAGAGCAAGT | 480 |
| QY | 4537 | GCGETTCCAGNTGGGATTGGGCCAAAACCCATTTAAGTAAAGGTTAGCAGAGCAAGT | 4572 |
| Db | | 481 GCGETTCCAGNTGGGATTGGGCCAAAACCCATTTAAGTAAAGGTTAGCAGAGCAAGT | 516 |


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RESULT 15
US-10-033-528-1233
; Sequence 1233, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Serist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1233

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| | Query Match | 8.9% | Score 516; | DB 12; | Length 516; |
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| | Best Local Similarity | 100.0%; | Prod. No. 4.3e-113; | | |
| | Matches 516; | Conservative | 0; | Mismatches 0; | Indels 0; |
| | | | | Gaps | 0; |
| QY | 4057 | AAAAGAATGACGGTTTACATATAAAATGTAATTAATCTATTGCTATATGCTATATGGAG | 4116 | | |
| Db | 1 | AAAAGAATGACGGTTTACATATAAAATGTAATTAATCTATTGCTATATGCTATATGGAG | 60 | | |
| QY | 4117 | TTGAAGGGAATACCTGTGCATAAGCCATATTCATAAATTAAGCATGAATAATATTCGCTAA | 4176 | | |

| | | | |
|----|------|---|------|
| Db | 61 | TTGAAGGGAATACTGTGCATTAAGCCAAATATGATAAATTAAGCATGAAAAAATATTGCTGAA | 120 |
| QY | 4177 | CTACTTTTGGTGCTTAAAGTTGFCACTATCTTGTAATTAGAGTTGCTCTACAATGACACA | 4236 |
| Db | 121 | CTACTTTTGGTGCTTAAAGTTGFCACTATCTTGTAATTAGAGTTGCTCTACAATGACACA | 180 |
| QY | 4237 | CAAAATCCCGCTAAATAAATTTATAAACAAGGGTCAATTCAAAATTTCAAGCTAAATGTTTTAGT | 4296 |
| Db | 181 | CAAAATCCCGCTAAATAAATTTATAAACAAGGGTCAATTCAAAATTTGAAGTAATGTTTTAGT | 240 |
| QY | 4297 | AAGGAGAGATTAGAAGACACACAGGCATAGCAATAGCATAGCTACCGATTAACTAATCG | 4356 |
| Db | 241 | AAGGAGAGATTAGAAGACACAGGCATAGCAATAGCATAGCTACCGATTAACTAATCG | 300 |
| QY | 4357 | GAACATGTAAACAGTTTACAAAATTAAGCAACTCTCCTTTGTCTTCAATGAAGCCC | 4416 |
| Db | 301 | GAACATGTAAACAGTTTACAAAATTAAGCAACTCTCCTTTGTCTTCAATGAAGCCC | 360 |
| QY | 4417 | TCATGTGCAGTAGAGATGCAGTTTCATCAAGAACAAACATCTCTTGCAAAATGGGTGTGAC | 4476 |
| Db | 361 | TCATGTGCAGTAGAGATGCAGTTTCATCAAGAACAAACATCTCTTGCAAAATGGGTGTGAC | 420 |
| QY | 4477 | GCGGTCCAGATGGATTGGCCAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAAAGT | 4536 |
| Db | 421 | GCGGTCCAGATGGATTGGCCAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAAAGT | 480 |
| QY | 4537 | GCGGTGCTTTAGTGTGCTGTGGCCGTTGTGGCGT | 4572 |
| Db | 481 | GCGGTGCTTTAGTGTGCTGTGGCCGTTGTGGCGT | 516 |

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Job time : 242 secs

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RESULT 15
US-10-033-528-1233
; Sequence 1233, Application US/10033528
; Patent NO. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033.528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1233

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|-----------------------|-----------------|--|-----------|-------------|
| Query Match | 8.9% | Score 516; | DB 12; | Length 516; |
| Best Local Similarity | 100.0%; | Pred. No. 4.3e-113; | | |
| Matches 516; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 4057 | AAAAGAATGCGTTTACATATAAAATCTAATTACTTATTCTGTATATGGAG | 4116 | |
| | | | | |
| Db | 1 | AAAAGAATGCGTTTACATATAAAATCTAATTACTTATTCTGTATATGGAG | 60 | |
| | | | | |
| QY | 4117 | TTGAAGGGAATCTCTGCATAAGCCATTATGATAAAATTAAGCATGAAAAATATTGCTGAA | 4176 | |
| | | | | |

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2002, 00:18:49 ; Search time 4857 Seconds
(without alignments)
19286.534 Million cell updates/sec

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Perfect score: 5784
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: em_estov:*

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8: em_htc:*

9: gb_esti:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_root:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 791.8 | 13.7 | 891 | 14 BQ925776 | BQ925776 AGENCOURT |
| 3 | 749.2 | 13.0 | 937 | 14 BQ934054 | BQ934054 AGENCOURT |
| 4 | 736 | 12.7 | 904 | 14 BQ940133 | BQ940133 AGENCOURT |
| 5 | 712.2 | 12.3 | 794 | 13 B1758564 | B1758564 603023071 |
| 6 | 700.2 | 12.1 | 876 | 9 AU121101 | AU121101 AU121101 |

| | | | | | | |
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| 7 | 694.8 | 12.0 | 721 | 14 | BM718851 | BM718851 UI-E-EO1- |
| c | 883.4 | 11.8 | 793 | 9 | AI346330 | AI346330 qp50a08.x |
| 8 | 682.8 | 11.8 | 748 | 12 | BG680063 | BG680063 602628211 |
| c | 675.8 | 11.7 | 756 | 12 | BQ008487 | BQ008487 UI-H-ED1- |
| c | 663.2 | 11.5 | 706 | 12 | BF109743 | BF109743 7168c12.x |
| c | 649 | 11.2 | 693 | 10 | BE673014 | BE673014 7d26h06.x |
| c | 645.2 | 11.2 | 660 | 9 | AA149866 | AA149866 z147g10.r |
| 13 | 638.8 | 11.0 | 661 | 13 | BM272400 | BM272400 1940d09.y |
| c | 635.8 | 11.0 | 673 | 14 | BQ002730 | BQ002730 UI-H-E11- |
| c | 632.6 | 10.9 | 706 | 10 | AW190828 | AW190828 x142c04.x |
| c | 629.8 | 10.9 | 651 | 13 | BG939270 | BG939270 cn31e12.x |
| c | 623.2 | 10.8 | 718 | 9 | AI453687 | AI453687 tj39a07.x |
| c | 620.2 | 10.7 | 658 | 9 | AA149859 | AA149859 z147e10.r |
| c | 617.6 | 10.7 | 642 | 14 | BQ019822 | BQ019822 UI-H-ED0- |
| c | 609.8 | 10.5 | 708 | 14 | BM997135 | BM997135 UI-H-ED0- |
| c | 609 | 10.5 | 817 | 13 | B1523839 | B1523839 603051961 |
| c | 608.8 | 10.5 | 637 | 9 | AA625208 | AA625208 af70f01.r |
| c | 608.8 | 10.5 | 660 | 14 | BM988626 | BM988626 UI-H-DH0- |
| c | 600.4 | 10.4 | 655 | 14 | BM971657 | BM971657 UI-H-DH0- |
| c | 600 | 10.4 | 648 | 9 | AI571506 | AI571506 tr85a06.x |
| c | 588 | 10.2 | 634 | 14 | BM998451 | BM998451 UI-H-DT1- |
| c | 583.8 | 10.1 | 615 | 14 | BQ003584 | BQ003584 UI-H-E11- |
| c | 580.8 | 10.0 | 630 | 14 | BQ017657 | BQ017657 UI-H-ED0- |
| c | 579 | 10.0 | 603 | 9 | AL703695 | AL703695 DKEZp686C |
| c | 567.8 | 9.8 | 631 | 13 | BG939446 | BG939446 cf53a03.x |
| c | 567 | 9.8 | 686 | 9 | AI417180 | AI417180 tg75g04.x |
| c | 565.8 | 9.8 | 642 | 10 | AW518826 | AW518826 ha44a06.x |
| c | 563.4 | 9.7 | 628 | 10 | BE221110 | BE221110 hu21a03.x |
| c | 561 | 9.7 | 652 | 9 | AA156875 | AA156875 z118f07.r |
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| c | 550.4 | 9.5 | 635 | 13 | BG939271 | BG939271 cn31e12.y |
| c | 547.4 | 9.5 | 557 | 10 | AW237648 | AW237648 xm75a06.x |
| c | 537.6 | 9.3 | 738 | 12 | BG751055 | BG751055 602729845 |
| c | 533.4 | 9.2 | 662 | 9 | AL048366 | AL048366 DKEZp586E |
| c | 528 | 9.1 | 565 | 9 | AA993886 | AA993886 ou02h10.s |
| c | 525.4 | 9.1 | 950 | 14 | BQ958014 | BQ958014 AGENCOURT |
| c | 525 | 9.1 | 656 | 12 | BF023089 | BF023089 ux04b06.y |
| c | 523.2 | 9.0 | 546 | 12 | BF593831 | BF593831 nac05e10. |
| c | 522 | 9.0 | 590 | 10 | AW385593 | AW385593 RC3-LT002 |

ALIGNMENTS

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| RESULT 1 | BO9333301 | 939 bp | linear | EST 21-AUG-2002 |
| BO9333301 | AGENCOURT 8744271 | Lupski_sciatic_nerve | Homo sapiens | CDNA clone |
| LOCUS | IMAGE:6205936 5', mRNA sequence. | | | |
| DEFINITION | BO9333301 | | | |
| ACCESSION | BO9333301 | | | |
| VERSION | BO9333301.1 | GI:22348684 | | |
| KEYWORDS | EST. | | | |
| SOURCE | human. | | | |
| ORGANISM | Homo sapiens | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| AUTHORS | 1 (bases 1 to 939) | | | |
| TITLE | NIH-MGC http://mgc.nci.nih.gov/. | | | |
| JOURNAL | National Institutes of Health, Mammalian Gene Collection (MGC) | | | |
| COMMENT | Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. James R. Lupski CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM13629 row: j column: 17 High quality sequence stop: 686. | | | |
| FEATURES | Location/Qualifiers | | | |
| source | 1..939 | | | |


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Db 1 AAATTAAGCATGAAATAATTTGCTGAACACTACTTTTGGTGTAAAGTTGTCACATATCTT 60
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Db 61 GAATTAGAGTTGCTCTACAATGACACACAATAATCCCATTAATAAATATTAACAAGGTC 120
QY 4270 AATTCAAAATTTGAAGTAATGTTTGTAGTAAGGAGATTTAGAAGACACAGCATAGCAAA 4329
Db 121 AATTCAAAATTTGAAGTAATGTTTGTAGTAAGGAGATTTAGAAGACACAGCATAGCAAA 180
QY 4330 TGACATAAGCTACCGATTAACTAATCGGAACATGTAACACAGTTTACAAAATAAACAAC 4389
Db 181 TGACATAAGCTACCGATTAACTAATCGGAACATGTAACACAGTTTACAAAATAAACAAC 240
QY 4390 TCTCCTCTTGTCTACAAATGAAGCCCTCATGTGCATAGAGATGAGATGATCAATCAAGA 4449
Db 241 TCTCCTCTTGTCTACAAATGAAGCCCTCATGTGCATAGAGATGAGATGATCAATCAAGA 300
QY 4450 ACAACATCTCTGCAAAATGGGTGACGCGTTCCACATGTTGATTTGGCAAAACCTCAT 4509
Db 301 ACAACATCTCTGCAAAATGGGTGACGCGTTCCACATGTTGATTTGGCAAAACCTCAT 360
QY 4510 TTAAGTAAAGTTAGCAGACCAAGTGCCTGCTTTAGTCTGCTGCTGCTGCTGCTGCTG 4569
Db 361 TTAAGTAAAGTTAGCAGACCAAGTGCCTGCTTTAGTCTGCTGCTGCTGCTGCTGCTG 420
QY 4570 CGTGGGGAGGCTCCTGCCCTGAGCTTCCCTCCAGCTTTGCTGCCCTGAGAGAACCA 4629
Db 421 CGTGGGGAGGCTCCTGCCCTGAGCTTCCCTCCAGCTTTGCTGCCCTGAGAGAACCA 480
QY 4630 GCAGACGACAGCGCGGAAAGGCGCATCTAACCGTATCTAGCTTTGTTAAGTGGGA 4689
Db 481 GCAGACGACAGCGCGGAAAGGCGCATCTAACCGTATCTAGCTTTGTTAAGTGGGA 540
QY 4690 CAAGTCTCTTTTACCTGATTGATGATACATTTTCAATTAAGGTTCCAGTTTAAATATTT 4749
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QY 4750 GTTAATATTTTAAAGTACATAGATAGAAATGCAATCTCCATTTACCAAGTAACTATTTAAAT 4809
Db 601 GTTAATATTTTAAAGTACATAGATAGAAATGCAATCTCCATTTACCAAGTAACTATTTAAAT 660
QY 4810 ATGCTAGTAAACATATGATGATATTAATTTCTAGAAACACATCTTAATAGTATATAAT 4869
Db 661 ATGCTAGTAAACATATGATGATATTAATTTCTAGAAACACATCTTAATAGTATATAAT 720
QY 4870 -CTGTGAAATATGAGCTTTGATAATATTAGGTTGTACGATGAAGCATGCTAGAGCT 4928
Db 721 CCCTGTGAAATATGAGCTTTGATAATATTAGGTTGTACGATGAAGCATGCTAGAGCT 780
QY 4929 GTACAGAAATACATAGA-GAATAATGAGGAGTTTATGATGAAACCTTAAATATA 4982
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RESULT 3
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DEFINITION AGENCOURT_881273 Lupski_sciatic_nerve Homo sapiens cdna clone
IMAGE:6202836 5', mRNA sequence.
ACCESSION BQ934054
VERSION BQ934054.1 GI:22349437
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 937)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, ph.D.
Email: c9apbs-i@mail.nih.gov
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Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUAM13621 row: i column: 13
High quality sequence stop: 613.
Location/Qualifiers
source
1. 937
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:6202836"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCTCG-3' and
5'-GACTAGTCTAGTCGCGAGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 310 a 172 c 185 g 269 t 1 others
ORIGIN

Query Match 13.0%; Score 749.2; DB 14; Length 937;
Best Local Similarity 99.0%; Pred. No. 2.3e-133;
Matches 754; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4125 AATACTGTGATAGCCATTAATTAAGCATGAAATAATTTGCTGAACACTACTTTT 4184
Db 1 AATACTGTGATAGCCATTAATTAAGCATGAAATAATTTGCTGAACACTACTTTT 60
QY 4185 GGTGCTTAAAGTTGCTACTATTTGAAATAGAGTTGCTCTACAAATGACACAAATCCC 4244
Db 61 GGTGCTTAAAGTTGCTACTATTTGAAATAGAGTTGCTCTACAAATGACACAAATCCC 120
QY 4245 GCTAAATAAATTAACAAGGGTCAATTTCAAAATTTGAAGTAATTTTAGTAAGGAGAG 4304
Db 121 GCTAAATAAATTAACAAGGGTCAATTTCAAAATTTGAAGTAATTTTAGTAAGGAGAG 180
QY 4305 ATTAGAGACAAACAGGATGACAAATGACATAGCTACCGATTAACATCGGAACATGT 4364
Db 181 ATTAGAGACAAACAGGATGACAAATGACATAGCTACCGATTAACATCGGAACATGT 240
QY 4365 AAAACAGTTACAAAATAAAGCAACTCTCTCTGCTCTACAAATGAAAGCCCTCATGTC 4424
Db 241 AAAACAGTTACAAAATAAAGCAACTCTCTCTGCTCTACAAATGAAAGCCCTCATGTC 300
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Db 301 AGTAGAGATGAGTTTCAATCAAAAGAACAAACATCCTTCAAAATGGGTGTGACGCGGTTCC 360
QY 4485 AGATGTGGATTTGGCAAAACCTCATTTAAGTAAAGGTTAGCAGAGCAAGATGCGGTGCT 4544
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QY 4545 TTAGCTGCTGCTGCTGCGTTGTGGCGTGGGAGGCTCTCTGCTGCTGCTCTCTCTCCCA 4604
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QY 4605 GCTTTGCTGCTGAGAGGAACAGCAGACAGCGCCGCGGAAAGGCGCATCTTAAGCC 4664
Db 481 GCTTTGCTGCTGAGAGGAACAGCAGACAGCGCCGCGGAAAGGCGCATCTTAAGCC 540
QY 4665 GTATCTAGGCTTTGGTAACTCGGACAAAGTTGCTTTTACCTGATTTGATGATACATTTCA 4724

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Db 541 GTATAGGCTTTGGTAAGTTCGGACAAAGTTCCTTTACCTGATTGATGATACATTTCA 600
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Db 601 TTAAGGTTCCAGCTTATAAATATTTTGGTTAAATATTTTAAAGTGACTATAGAATGCAACTC 560
QY 4785 CATTTACCAGTAACTATTTTAAATATGCTAGTAGTAAACACATATGATGATATATTTCTAGA 4844
Db 661 CATTTACCAGTAACTATTTTAAATATGCTAGTAGTAAACACATATGATGATATATTTCTAGA 720
QY 4845 AACAACATCTAATAGTATATATTAATCCCTGTGAAATATGAGG 4886
Db 721 AACAACATCTAATAGTATATATTAATCCCTGTGAAATATGAGG 762

RESULT 4
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LOCUS AGENCOURT_8784556 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6376342
DEFINITION 5', mRNA sequence.
ACCESSION BO940133
VERSION BO940133.1 GI:22355611
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN2558 row: f column: 23
High quality sequence stop: 551.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6376342"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pOTB7; Site: 1; XhoI; Site: 2;
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCACGAC(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. 1"
BASE COUNT 237 a 243 c 249 g 173 t 2 others
ORIGIN
Query Match 12.7%; Score 736; DB 14; Length 904;
Best Local Similarity 99.6%; Pred. No. 7.9e-131;
Matches 747; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2450 CGATGCTGTGATGATGACGATGACATGACGGTGTGACCGATGAGAGGACAACTGCCA 2509
Db 1 CGATGCTGTGATGATGACGATGACATGACGGTGTGACCGATGAGAGGACAACTGCCA 60
QY 2510 GCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGTGGGACCGCTGTGA 2569
Db 61 GCTCCTCTTCAATCCCGCCAGGCTGACTATGACAAGGATGAGTGGGACCGCTGTGA 120

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QY 2570 CAACTGCCCTTACGTGACCAACCCCTGCCAGATCGACAGACAAACAATGGAGGGTGA 2629
Db 121 CAACTGCCCTTACGTGACCAACCCCTGCCAGATCGACAGACAAACAATGGAGGGTGA 180
QY 2630 CGCTGCTCCGTGGACATTTGATGGGAGCGATGCTTCAATGAACGAGACAATTTGCCCTA 2689
Db 181 CGCTGCTCCGTGGACATTTGATGGGAGCGATGCTTCAATGAACGAGACAATTTGCCCTA 240
QY 2690 CGTCTACAACTGACACGAGGACACGATGCTGACGCTGTGGGGATCACTGTGACAA 2749
Db 241 CGTCTACAACTGACACGAGGACACGATGCTGACGCTGTGGGGATCACTGTGACAA 300
QY 2750 CTGCCCCCTGTGTGCAACCCCTGACGACGACCGACGATGACCTTTGTTGGGACCA 2809
Db 301 CTGCCCCCTGTGTGCAACCCCTGACGACGACCGACGATGACCTTTGTTGGGACCA 360
QY 2810 GTGTGACAAACGAGGACATAGATGACGCGCCACCAACGACCACTGACCTGCCC 2869
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QY 2870 CTACATCTCCAAACGCGCTGACCATGACAGACGCGCCAGGCGACGCTGTGA 2929
Db 421 CTACATCTCCAAACGCGCTGACCATGACAGACGCGCCAGGCGACGCTGTGA 480
QY 2930 CCTGATGATGACAAACGATGGCTCCCGATGACAGGACAACTGCCGCTTGTGTTCAA 2989
Db 481 CCTGATGATGACAAACGATGGCTCCCGATGACAGGACAACTGCCGCTTGTGTTCAA 540
QY 2990 CCCAGACGAGGACTTGGAGCGGTGATGGAGCGGGGTGATTTGTAAGATGATTTGA 3049
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QY 3110 AGACTTCAGGAACCTCCAGATGGTCCCTTGGATCCCAAGGAGGACCA-CCCAAAATTTGATC 3168
Db 661 AGACTTCAGGAACCTCCAGATGGTCCCTTGGATCCCAAGGAGGACCA-CCCAAAATTTGATC 720
QY 3169 CCAACTGGGTGATTCGCCATCAAGCAAGG 3198
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RESULT 5
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LOCUS 603023071F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5193785 5',
DEFINITION mRNA sequence.
ACCESSION BO940133
VERSION BO940133.1 GI:15750142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 794)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN1484 row: m column: 18
High quality sequence start: 29

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QY 3408 GCCTATGGCTACTCCGGCGTGTCCCTCAAGGTGGTGAACCTCACCACGGGGACGGCGAG 3467
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Db 421 CACCTGAGGAACCGCTGTGGGCACACGGGGAACACCGCGGGCAGGTGCGAACCTTATGG 480
QY 3528 CACGACCCCGAGGAACATTTGGCTGGAAGGACTACACGGGCTATAGTGGCACCTGACTCAC 3587
Db 481 CACGACCCCGAGGAACATTTGGCTGGAAGGACTACACGGGCTATAGTGGCACCTGACTCAC 540
QY 3588 AGGCCACAGACCGGTACATCAGAGTCTTAGTGATGAAAGAAAACAGTCAATGCGCAGAC 3647
Db 541 AGGCCACAGACTGGGTACATCAGAGTCTTAGTGATGAAAGAAAACAGTCAATGCGCAGAC 600
QY 3648 TCAGGACCTATCTATGACCAACCTTACGCTGCGGGCGGCTGGGCTATTGCTCTTCTCT 3707
Db 601 TCAGGACCTATCTATGACCAACCTTACGCTGCGGGCGGCTGGGCTATTGCTCTTCTCT 660
QY 3708 CAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCAGAGAT 3752
Db 661 CAAGAAATGGTCTATTCTCAGACCTCAAGTACGAATGCAGAGAT 705

RESULT 7
BM718851
LOCUS
DEFINITION
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  UI-E-EO1-a-jc-j-23-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
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ACCESSION
  BM718851
VERSION
  BM718851.1 GI:19037242
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 721)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  9704477
  Contact: Soares, MB
  Program for Rat Gene Discovery and Mapping
  University of Iowa
  451 Eckstein Medical Research Building Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: msoares@blue.weeg.uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
  Location/Qualifiers
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      /db_xref="taxon:9606"
      /clone="UI-E-EO1-a-jc-j-23-0-UI"
      /clone_lib="UI-E-EO1"
      /tissue_type="fetal eye"
      /dev_stage="fetal"
      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
      /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
      modified polylinker; Site_1: EcoR I; Site_2: Not I;
      UI-E-EO1 is a normalized cDNA library containing the
      following tissue(s): fetal eye. The library was
      constructed according to Bonaldo, Lennon and Soares,
      Genome Research, 6:791-806, 1996. First strand cDNA
      synthesis was primed with an oligo-dT primer containing a

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Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(drr)18 tail. The sequence tag for this library is
GCGGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
BASE COUNT      238 a      123 c      156 g      204 t
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Query Match      12.0%; Score 694.8; DB 14; Length 721;
Best Local Similarity 99.4%; Pred. No. 6.4e-123;
Matches 718; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
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Db 1 GCCTTCAGAGGATAATATCAATGAACTCAGAGATGAACATCTAACCCACCTAGAGGAA 60
QY 3980 ACCAGTTCGGTGATATGAGACTTTTATGAGTGAGTGAATAATGGGCATGCCATTTACATGG 4039
Db 61 ACCAGTTCGGTGATATGAGACTTTTATGAGTGAGTGAATAATGGGCATGCCATTTACATGG 120
QY 4040 CTTTTCCTGTTGTTTAAAGAAATGACGTTTACATATAAAATGTAATTAATTTACTTATTGTA 4099
Db 121 CTTTTCCTGTTGTTTAAAGAAATGACGTTTACATATAAAATGTAATTAATTTACTTATTGTA 180
QY 4100 TTTATGCTATATGAGTGTGAAGGAATGACTGTGCTAAGGCATTTATGATAAATTAAGCA 4159
Db 181 TTTATGCTATATGAGTGTGAAGGAATGACTGTGCTAAGGCATTTATGATAAATTAAGCA 240
QY 4160 TGAAAAATATTGCTGAACACTACTTTTGGTGGCTTAAAGTGTCTCACTATTCTTGAATTAGAGT 4219
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QY 4220 TGCTCTACAATGACACACAAATCCCGCTTAAATAAATTAACAAGGTCATTAATCAAAAT 4279
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QY 4280 TGAAGTAAATGTTTAAAGGAGAGATTAGAGACACAGGCATAGCAATGACATAGC 4339
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QY 4340 TACCGATTAACTAATCGGAACATGTAAACACAGTTTACAAAAATTAACAGCACTCTCCTCTTG 4399
Db 421 TACCGATTAACTAATCGGAACATGTAAACACAGTTTACAAAAATTAACAGCACTCTCCTCTTG 480
QY 4400 TCCTACAATGAAGCCCTCATGTGCGAGTAGAGATGCGATTTTCATCAAAAGACAAACATCC 4459
Db 481 TCCTACAATGAAGCCCTCATGTGCGAGTAGAGATGCGATTTTCATCAAAAGACAAACATCC 540
QY 4460 TTGCAATGGGTGTGACGCGGTTCAGATGCGATTTGCGAAACCTCATTTAAGTAAAA 4519
Db 541 TTGCAATGGGTGTGACGCGGTTCAGATGCGATTTGCGAAACCTCATTTAAGTAAAA 600
QY 4520 GGTTAGCAGACCAAGTCCGCTGCTTTAGCTGCTGCTTGTGCGCTTGTGGCGTCCGGGAG 4579
Db 601 GGTTAGCAGACCAAGTCCGCTGCTTTAGCTGCTGCTTGTGCGCTTGTGGCGTCCGGGAG 660
QY 4580 GCTCCTGCCTGAGCTTCCTCCAGCTTTGCTGCCTGAGAGAACACAGCAGACGAC 4639
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QY 4640 AG 4641
Db 720 AG 721
RESULT 8
AI346330/c
LOCUS
DEFINITION
  qp50808.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926422 3'
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  AI346330

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Best Local Similarity: 97.3%; Pred. No. 1.3e-120; Mismatches 0; Indels 8; Gaps 3;

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Db 61 CAATCCATTTACCAGTAACTATTTTAAATATGCTAGTACACATATGTAGTATAAT 120
QY 4839 TCTAGAAACAAACATCTAATAAGTATATAATCTGTGAATAATAGAGCTTATATATT 4898
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Db 121 TCTAGAAACAAACATCTAATAAGTATATAATCTGTGAATAATAGAGCTTATATATT 180
QY 4899 AGGTGTCTACAGTGAAGCATGCTAGAACGCTGTAACAGATACATAGAGATAATAGGAG 4958
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Db 181 AGGTGTCTACAGTGAAGCATGCTAGAACGCTGTAACATATACATAGAGATAATAGGAG 240
QY 4959 TTTATGATGGAACCTTAATATATATATGTTGCCAGGATTTTGTCAATATTTGTACTG 5018
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QY 5019 TTATCTATCTGCTATATGGAATCTTTTAAATCAAAAGCTGAAACGAAATCAGCATTT 5078
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Db 301 TTATCTATCTGCTATATGGAATCTTTTAAATCAAAAGCTGAAACGAAATCAGCATTT 360
QY 5079 AGTCTTGCCAGGCACACCAATCAATCAGTCATGTGTATATGCAAAAGTTTGTGTTTGT 5138
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Db 361 AGTCTTGCCAGGCACACCAATCAATCAGTCATGTGTATATGCAAAAGTTTGTGTTTGT 420
QY 5139 TTTGTTTTTTTTT-----GTTGTTGGTTTTTTTTTAAAGTTGCAATGATCTTCGAG 5193
|||||
Db 421 TTTGTTTTTTTTTAAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
QY 5194 GAAATAGTCATCTATCCACTCCACATAGGGGTTTGTAGTAAAGAGAGTCTGCTCTGA 5253
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Db 481 GAAATAGTCATCTATCCACTCCACATAGGGGTTTGTAGTAAAGAGAGTCTGCTCTGA 540
QY 5254 TGATGATAGGGGGCAATCTTTTCCCTTTCTGTTTAAATGATCATCATCTTCTATGCC 5313
|||||
Db 541 TGATGATAGGGGGCAATCTTTTCCCTTTCTGTTTAAATGATCATCATCTTCTATGCC 600
QY 5314 AAACAGGAACGATCAATACCTTTAGTCTTAATGATACATTCATTCATTAATAATTAAT 5373
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Db 601 AAACAGGAACGATCAATACCTTTAGTCTTAATGATACATTCATTCATTAATAATTAAT 660
QY 5374 TTTGTTGTTTCTTTGAGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5431
|||||
Db 661 TTTGTTGTTTCTTTGAGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720
QY 5432 GCGTGTGGAGCTG-TATTCCCGAGACAA 5458
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Db 721 GCGTGTGGAGCTGTTATTCCCGAGACAA 748

RESULT 10
BQ008487/c
LOCUS
DEFINITION UI-H-ED1-ayk-b-03-0-UI-s1 NCLCGAP_ED1 Homo sapiens CDNA clone
IMAGE:5839778 3', mRNA sequence.
ACCESSION BQ008487
VERSION BQ008487.1 GI:19733388
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NCI-Base
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 637-685, >(CAAA)n#simple_repeat
Seq primer: M13 FORWARD
POLYA-Yes.

FEATURES
source

Location/Qualifiers
1..756

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5839778"
/clone_lib="NCLCGAP_ED1"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCLCGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C8S. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_L1B=UI-H-ED1
TAG_ISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"

BASE COUNT 280 a 145 c 117 g 213 t 1 others
ORIGIN

Query Match 11.7%; Score 675.8; DB 14; Length 756;
Best Local Similarity 98.4%; Pred. No. 2.8e-119;
Matches 726; Conservative 0; Mismatches 3; Indels 9; Gaps 4;

QY 5056 ACGCTGAAAACGAATCAGCATTTAGTCTTGCCAGGCACACCAATAATCAGTCATGTGA 5115
|||||
Db 756 ACGCTGAAAACGAATCAGCATTTAGTCTTGCCAGGCACACCAATAATCAGTCATGTGA 697
QY 5116 ATATGCAC-AAAGTTGTTTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 5170
|||||
Db 696 ATATGCACAAAGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTT 637
QY 5171 TAAAGTTGATGATCTTCTGCGAGGAATAGTCATCTCCACTCCACATAGAGGGTTTA 5230
|||||
Db 636 TAAAGTTGATGATCTTCTGCGAGGAATAGTCATCTCCACTCCACATAGAGGGTTTA 577
QY 5231 TAAAGAGAGTCTGCTGCTGATGATGATGAGGGGCAAAATCTTTTCCCTTTCTGTT 5290
|||||
Db 576 TAAAGAGAGTCTGCTGCTGATGATGATGAGGGGCAAAATCTTTTCCCTTTCTGTT 517
QY 5291 AATAGTATCATATTTCTTATGCCAAACAGGACGATCCATACCTTTAGTCTTTAATGTACA 5350
|||||
Db 516 AATAGTATCATATTTCTTATGCCAAACAGGACGATCCATACCTTTAGTCTTTAATGTACA 457
QY 5351 CATTCATTTGATAAAATTAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 5407
|||||
Db 456 CATTCATTTGATAAAATTAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 397
QY 5408 TTTTGTCTGACTTTTACTTTTTCGTCGTGAGCTGTATTCCCGAGACCAACGAAGCGT 5466
|||||
Db 396 TTTTGTCTGACTTTTACTTTTTCGTCGTGAGCTGTATTCCCGAGACCAACGAAGCGT 337

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QY 5467 TGGATACCTTCATTAATGTAGCAGCTGCTCAACAGCGTCGAGGCTTTCTCTGTTCTGTT 5526
Db 336 TGGATACCTTCATTAATGTAGCAGCTGCTCAACAGCGTCGAGGCTTTCTCTGTTCTGTT 277
QY 5527 GTGGGTCAACCGTACAAATGCTGGGAATGACGATGATGTAATATTTAGAAATGACCA 5586
Db 276 GTGGGTCAACCGTACAAATGCTGGGAATGACGATGATGTAATATTTAGAAATGACCA 217
QY 5587 TATTTTGTGAATATTTATGTTTTTCTAAACAAATTTATCGATAGGTTGATGAAACG 5646
Db 216 TATTTTGTGAATATTTATGTTTTTCTAAACAAATTTATCGATAGGTTGATGAAACG 157
QY 5647 TCATGCTTTTGGCAAGAGCTGTAATATTTATTTATGTTGTCACATGGTCACAAATTTCA 5706
Db 156 TCATGCTTTTGGCAAGAGCTGTAATATTTATTTATGTTGTCACATGGTCACAAATTTCA 97
QY 5707 CCAGTGAACCCCTGCACTTACGTAGAACCTCACTTTTAAAGATTAAACACAGGAATAAA 5766
Db 96 CCAGTGAACCCCTGCACTTACGTAGAACCTCACTTTTAAAGATTAAACACAGGAATAAA 37
QY 5767 TTGTAAAAAGGTTTCT 5784
Db 36 TTGTAAAAAGGTTTCT 19

RESULT 11
BF109743/c
LOCUS
DEFINITION
7168c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3526654.3' similar to SW:TSPI_BOVIN Q28178 THROMBOSPONDIN 1
; mRNA sequence.
BF109743
BF109743.1 GI:10939433
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapps-femail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from G1bco
High quality sequence stop: 470.
FEATURES
source
1..706
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3526654"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSP pool 1:
309384-310919, 323208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
738280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
208 a 138 c 153 g 206 t 1 others
BASE COUNT
```

ORIGIN

```
Query Match 11.5%; Score 663.2; DB 12; Length 706;
Best Local Similarity 97.2%; Pred. No. 7.3e-117;
Matches 685; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 3573 TGGCACCTGACTCACAGCCCAAGACCGGTACATCAGAGTCTTAGTCATGAAGGAAA 3632
Db 706 TGGCACCTGACTCCAGGCCCAAGACTGGTACCATCAGAGTCTTAGTCATGAGGAATC 647
QY 3633 CAGGTCTATGGCAGACTCAGGACCTATCTATGACCAAACTACGCTGGCGGCGGTGGT 3692
Db 646 CAGGTCTATGGCAGACTCAGGACCTAT-TATACCCAACTACGCTGGCGGCGGTGGT 588
QY 3693 CTATTTGCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAGAT 3752
Db 587 CTATTTGCTTCTCTCAAGAAATGGTCTATTTCTCAGACCTCAAGTACGAGAT 528
QY 3753 ATTTAAACAAGATTTGCTGCAATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACA 3812
Db 527 ATTTAAACAAGATNTGCTGCAATTTCCGGCAATGCCCTGTGCATGCCATGGTCCCTAGACA 468
QY 3813 CCTCAGTTTCATTTGGTCTTGGCGCTTCTCTCTAGCAGCACCTCCTGTCCCTTGACC 3872
Db 467 CCTCAGTTTCATTTGGTCTTGGCGCTTCTCTCTAGCAGCACCTCCTGTCCCTTGACC 408
QY 3873 TTAACCTCTGATGGTTCTTCACTCTGCGCAGCAACCCCAACCCCAAGTGCCTTCAGAGGA 3932
Db 407 TTAACCTCTGATGGTTCTTCACTCTGCGCAGCAACCCCAACCCCAAGTGCCTTCAGAGGA 348
QY 3933 TAAATATCAATGGAACCTCAGAGATGACATCTAACCCACTAGAGAAACCAAGTTGGTGA 3992
Db 347 TAAATATCAATGGAACCTCAGAGATGAACATCTAACCCACTAGAGAAACCAAGTTGGTGA 288
QY 3993 TATATGAGACTTTATGTGGAGTGAATAATGGGCATGCCATTACATTCGTTTTCTGTTT 4052
Db 287 TATATGAGACTTTATGTGGAGTGAATAATGGGCATGCCATTACATTCGTTTTCTGTTT 228
QY 4053 GTTTAAAAAAGAAATGACGTTTACATATAAAATGTAATTAATTAATTTATGTTATAT 4112
Db 227 GTTTAAAAAAGAAATGACGTTTACATATAAAATGTAATTAATTAATTTATGTTATAT 168
QY 4113 GGAGTTGAAGGAATGCTGTCATAGCCATTATGATAAATTAAGCATGAAATATTTGC 4172
Db 167 GGAGTTGAAGGAATGCTGTCATAGCCATTATGATAAATTAAGCATGAAATATTTGC 108
QY 4173 TGAACCTACTTTTGGTGTCTTAAAGTTGTCACATTTCTTGAATAGAGTTGCTCTACAATGA 4232
Db 107 TGAACCTACTTTTGGTGTCTTAAAGTTGTCACATTTCTTGAATAGAGTTGCTCTACAATGA 48
QY 4233 CACACAAATCCCGCTAAATAAATTTATAACAAGGTCATTAATCAAA 4277
Db 47 CACACAAATCCCATTAATAAATTTATAACAAGGTCATTAATCAAA 3
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RESULT 12
BE673014/c
LOCUS
DEFINITION
7426h06.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3248411 3'
similar to gb:L12350 THROMBOSPONDIN 2 PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION BE673014
VERSION BE673014.1 GI:10033555
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 693)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
```

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 462.

FEATURES

Location/Qualifiers
 1. .693
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NCI_CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 262 a 137 c 111 g 183 t

ORIGIN

Query Match 11.2%; Score 649; DB 10; Length 693;
 Best Local Similarity 98.1%; Pred. No. 3.9e-114;
 Matches 678; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY 5095 CCCAATATCAGTCATGTTGTAATATGCACAGTTTGTGTTTTGTTTTGTTTTGTTG 5154
 DB 693 CCCAATATCCAGTCATGTTGTAATATGCCCAAGTTTGTGTTTTGTTTTGTTT -GTA 636
 QY 5155 GTTGTTTTTGTCTTAAGTTGCATGCTCTTCGAGGAATAGTCACATCCCACT 5214
 DB 635 GTTGTTTTTGTGCTTTAAGTGGCATGATCTTTCGAGGAATAGTCACATCCCACT 576
 QY 5215 CCACATAAGGGTTTTAGTAAGAGAAGTCTGCTGCTGATGATGATAGGGGCAAACT 5274
 DB 575 CCACATAAGGGTTTTAGTAAGAGAAGTCTGCTGCTGATGATGATAGGGGCAAACT 516
 QY 5275 TTTTCCCTTCTGTTAATAGTCATCATCTTATGCCAAGACGATCCATAACT 5334
 DB 515 TTTTCCCTTCTGTTAATAGTCATCATCTTATGCCAAGACGATCCATAACT 456
 QY 5335 TAGTCTTAAGTACACATTCATTTTCATAAAATTAATTTGTTGTTCTCTTGAGGTT 5394
 DB 455 TAGTCTTAAGTACACATTCATTTTCATAAAATTAATTTGTTGTTCTCTTGAGGTT 396
 QY 5395 GATCGTTGTTGTTTCTGCTGCACATTTTACTTTTTTCGCTGAGCTGATATCCCGAG 5454
 DB 395 GATCGTTGTTGTTTCTGCTGCACATTTTACTTTTTTCGCTGAGCTGATATCCCGAG 336
 QY 5455 A-CACGAAGCGTTGGGATCTTCATTAATAGTAGCGACTGTCAACACGCGTGCAGTTTT 5513
 DB 335 ACCACGAAGCGTTGGGATCTTCATTAATAGTAGCGACTGTCAACACGCGTGCAGTTTT 276
 QY 5514 CTGTTTCTGTTGTTGGGCTCAACCGTACAATGTTGSGGAATGACGATGATGCAATAT 5573
 DB 275 CTGTTTCTGTTGTTGGGCTCAACCGTACAATGTTGSGGAATGACGATGATGCAATAT 216
 QY 5574 TTAGAATGTACCATATTTTTTTGTAATATTTATGTTTTTCTTAACAAATTTATCGTATA 5633
 DB 215 TTAGAATGTACCATATTTTTTTGTAATATTTATGTTTTTCTTAACAAATTTATCGTATA 156

QY 5634 GGTGATGAACGTCATGTTGTTTGCCTAAAGACTGTAAATATTTATTTATGTGTTCCACAT 5693
 DB 155 GTTGTGATGAACGTCATGTTGTTTGCCTAAAGACTGTAAATATTTATTTATGTGTTCCACAT 96
 QY 5694 GGTCAAAATTTCCACACCTGAAACCTGCACTTAGCTAGTAACTCACTTTTAAAGATTAAAC 5753
 DB 95 GGTCAAAATTTCCACACCTGAAACCTGCACTTAGCTAGTAACTCACTTTTAAAGATTAAAC 36
 QY 5754 AACAGGAATAAATTTGTAATAAAGGTTTTCT 5784
 DB 35 AACAGGAATAAATTTGTAATAAAGGTTTTCT 5

RESULT 13

AA149866

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Score

DB

Pred. No.

e-

Matches

Indels

Gaps

Length

Score

DB

Pred. No.

e-

Matches

Indels

Gaps

Length

Score

DB

Pred. No.

e-

Matches

Indels

Gaps

Length

Score

DB

Pred. No.

e-

Matches

Indels

Gaps

Length

Score

DB

Pred. No.

e-

RESULT 15
BQ002730/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ002730 673 bp mRNA linear EST 26-MAR-2002

UI-H-E11-ayv-c-13-0-UI.s1 NCI_CGAP_E11 Homo sapiens cDNA clone

IMAGE:5844036 3', mRNA sequence.

BQ002730

BQ002730.1 GI:19727630

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 673)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..673

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5844036"

/clone_lib="NCI_CGAP_E11"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)

with a modified polylinker; Site.1: EcoR I; Site.2: Not I;

NCI_CGAP_E11 is a normalized cDNA library containing the

following tissue(s): Chondrosarcoma. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dr primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into p7T3-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dr)18 tail. The sequence tag for this library is

ACACTGTCAC.

TAG_LIB=UI-H-E11

TAG_TISSUE=chondrosarcoma

TAG_SEQ=ACACTGTCAC"

BASE COUNT

ORIGIN

183 a 144 c 147 g 198 t 1 others

Query Match

Best Local Similarity

Matches 659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

11.0%; Score 635.8; DB 14; Length 673;

99.2%; Pred. No. 1.3e-111;

99.2%; Pred. No. 1.3e-111;

Qy 3505 CGGGCAGGTCGGAACCTTATGGCAGCAGCCAGGACATTGGCTGGAGGACTACACGG 3564

|||||

Db 673 CGGGCAGGTCGGAACCTTATGGCAGCAGCCAGGACATTGGCTGGAGGACTACACGG 614

|||||

Qy 3565 CCTATAGTGGCAGCTGACTCAGAGGCCAGCGGTACATCAGAGCTCTAGTGCATG 3624

|||||

Db 613 CCTATAGTGGCAGCTGACTCAGAGGCCAGCGGTACATCAGAGCTCTAGTGCATG 554

|||||

Qy 3625 AAGGAAACAGGTCATGGCAGACTCAGGACCTATCTATGACCAACCTACGCTGGCGGG 3684

|||||

Db 553 AAGGAAACAGGTCATGGCAGACTCAGGACCTATCTATGACCAACCTACGCTGGC-GGC 495

|||||

Search completed: December 27, 2002, 04:35:08
Job time : 4912 secs